

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 00:01:33 ; Search time 4609 Seconds  
(without alignments)

2153.516 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258

Sequence: 1 IIKGFECKPHSQPQALFE.....GYTVKVKYVDVIQETMKN 229

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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7	1258	100.0	1192	6	AR152174 Sequence
8	1258	100.0	1204	6	AX358932 Sequence
9	1258	100.0	1204	6	AX362425 Sequence
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# ALIGNMENTS

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 VERSION AX016287.1 GI:10041854  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.  
 Human casb12 polypeptide, a serine protease  
 Patent: WO 9949055-A 1 30-SEP-1999;  
 BRUCK CLAUDINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);  
 COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA  
 (BE)  
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 DB 293 CACTGCCTCAAGCCCGCTACATAGTTCACCTGGGCGAGCAGCAACCTCCAGAGGAGGAG 352  
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 KEYWORDS JP12002507425-A/1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (Bases 1 to 1106)  
 Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.  
 Human CASB 12 polypeptide, a serine protease  
 Patent: JP 2002507425-A 1 12-MAR-2002;  
 SMITHKLINE BEECHAM BIOLOGICALS SA  
 OS Homo sapiens (human)  
 PN JP 2002507425-A/1  
 PD 12-MAR-2002  
 PF 17-MAR-1999 JP 2000538015  
 PR 20-MAR-1998 GB 9806095.7  
 PI CLAUDINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI  
 CARLOTA VINALS BASSOLS  
 PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,  
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ACCESSION BD137020
VERSION BD137020.1 GI:10041855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 949055-A 3 30-SEP-1999; SMITHKLINE BEECHAM BIOLOG (BE);
COACHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
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RESULT 4
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LOCUS BD137020
DEFINITION Human CASB 12 polypeptide, a serine protease.
ACCESSION BD137020
VERSION BD137020.1 GI:23231965
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
TITLE Human CASB 12 polypeptide, a serine protease
JOURNAL Patent: JP 2002507425-A 2 12-MAR-2002;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Homo sapiens (human)
PN JP 2002507425-A/2
PD 12-MAR-2002
PF 17-MAR-1999 JP 2000538015
PR 20-MAR-1998 GB 9806095.7
PI CLAUDINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI
CARLOTA VINALS BASSOLS
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68,G01N33/15,
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 FT source 1. 1158  
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 Db 843 G A T C C G T G C G A T C A C C C A A A G C C T G G T G T C T A C C G A A G C T C G C A A A T A T G T G A C 902  
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 Db 903 T G G A T C C A G G A G A C G A T G A A G A C A A T 929  
 RESULT 5  
 LOCUS AB013730 1181 bp mRNA linear PRI 20-JUN-2000  
 DEFINITION Homo sapiens mRNA for Hippocampus, complete cds.

AB013730  
 VERSION GI:6681453  
 KEYWORDS Hippocampus. (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (sites)  
 Mitsui S., Yamada, T., Okui, A., Kominami, K., Uemura, H. and Yamaguchi, N.  
 TITLE A novel isoform of a kallikrein-like protease, TLSP/hippocastin, (PRSS20), is expressed in the human brain and prostate  
 JOURNAL Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)  
 PUBMED 10872828  
 REFERENCE 2 (bases 1 to 1181)  
 AUTHORS Yamaguchi, N. and Mitsui, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural University of Medicine, Res. Ins. Geriatrics; Kawarimachi Hirokoji, Kyoto, Kyoto 602-8566, Japan (E-mail: nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848, Fax:81-75-251-5848)  
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 /db\_xref="GI:6681454"  
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 Score: 1258.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AB013730 (1-1181)  
 Qy 1 l l e l l e l y s g l y p h e g l u c y s l y s p r o h i s s e r g l n p r o t r p g l n a l a l e u p h e g l u 20  
 Db 184 A T C A T C A A G G G G T T C G A G T C A A G C C T C A C T C C C A G C C C T G G C A G C A G C C T T T C G A G 243  
 Qy 21 L y s T h r A r g L e u L e u C y s G l y A l a T h r L e u L e u A l a P r o A r g T r p L e u L e u T h r A l a A l a 40  
 Db 244 A A G A C G C G G T A C T C T G T G G G C A G C G C T C A T C G C C C C A G A T G G C T C T G A C A G A G C C 303  
 Qy 41 H i s C y s L e u L y s P r o A r g T y r I l l e V a l H i s L e u G l y G l n H i s A s n L e u G l n L y s G l u G l u 60  
 Db 304 C A C T G C C T C A A G C C C G C T A C A T A G T T C A C T G G G C A G C A C A C C T C C A G A A G A G A G A G 363  
 Qy 61 G l y C y s G l u G l n T h r A r g T h r A l a T h r G l u S e r P h e P r o H i s P r o G l y P h e A s n A s n S e r 80  
 Db 364 G G C T G T G A G C A G A C C C G G A G C A C C A T G A C A T C A T G T G T G A A G A T G G C A T C G C A G T C T C C 423  
 Qy 81 L e u P r o A s n L y s A s p H i s A r g A s n A s p I l l e M e t L e u V a l L y s M e t A l a S e r P r o V a l S e r 100  
 Db 424 C T C C C C A A C A A G A C C A C C C A T G A C A T C A T G T G T G A A G A T G G C A T C G C A G T C T C C 483  
 Qy 101 I l e T h r T r p A l a V a l A r g P r o L e u T h r L e u S e r S e r A r g C y s V a l T h r A l a G l y T h r S e r 120



Db 484 ATCACTGGGCTGTGGACCCCTCACCCCTCTCTCACTGTGTCACTGTGTGGACACAGC 543  
Qy 121 CysLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 544 TGCCTCATTTCCGGCTGGGCGAGCACGCTCCAGCCGCCAGTTACGCTGCTCACACTTG 603  
Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyProGlyAsn 160  
Db 604 CGATGCCGCCAACATCACCATTTAGACACACAGAGTGTGAGAACGCTACCCCGGCAAC 663  
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
Db 664 ATCACACACACCATGGTGTGTCAGCGTGCAGGAGGGGCGAAGGACTCTCTCCAGGGT 723  
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200  
Db 724 GACTCCGGGGGCGCTCTGTGCTGTAAACAGCTCTTCAAGGCATTATCTCTCGGGGCCAG 783  
Qy 201 AspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyValAsp 220  
Db 784 GATCCGTTGCGATCACCCGAAAGCCTGGTGTCTACAGGAAGTCTGCAATATGTGGAC 843  
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229  
Db 844 TGGATCCAGGAGACGATGAAGACAAT 870

RESULT 6  
AB012917 1186 bp mRNA linear PRI 31-JAN-2003  
LOCUS Homo sapiens mRNA for serine protease (TLSP), complete cds.  
DEFINITION  
ACCESSION AB012917  
VERSION AB012917.1 GI:3649790  
KEYWORDS TLSP; serine protease (TLSP).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Yoshida S., Taniguchi M., Suemoto T., Oka T., He X. and Shiozaka S.  
cDNA cloning and expression of a novel serine protease, TLSP  
Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)  
98438738  
PUBMED 9765601  
REFERENCE 2 (bases 1 to 1186)  
Yoshida S.  
Direct Submission  
Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1,  
Asahikawa Medical College, Midorigaoka Higashi 2-1-1, Asahikawa,  
Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp,  
Tel: 81-166-68-2300, Fax: 81-166-68-2309)  
Tel: 81-166-68-2300, Fax: 81-166-68-2309)  
Location/Qualifiers  
1. .1186  
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26. .874  
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/db\_xref="GI:3649791"  
TRANSLATION="MORLEWRDKSSGRLTAKEPGARSSPLOWRILQILILALA  
TGLVGETRIIKGFEKPKSPQWQAALFEKRLLOGATILAPRLWLTAAHCLKPRIV  
HLCQHNLEKEGCEQRTATESPFPGFNNSLPNKDRNDIMLVKNASPVSIWVRP  
LTLSRCVTAGTSCSLISGWGSTSSPOLRPLTLCANITIIIEHQENAYPGNITDTM  
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polyA\_signal 1164. .1169  
polyA\_site 1186  
/note="12 a nucleotides"

ORIGIN

Alignment Scores:  
Pred. No.: 4, 85e-97 Length: 1186  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-856-320A-2\_COPY\_54\_282 (1-229) x AB012917 (1-1186)  
Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20  
Db 185 ATCATCAGGGGTTTCAGAGTGCAGGCTCCTCCAGCCCTGGCAGGAGCCCTGTTCAG 244  
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThraAla 40  
Db 245 AAGACGGCGTACTCTGTGGGGCGACGCTCATCGCCCCAGATGGCTCTCCAGCAGCC 304  
Qy 41 HisCysLeuLysProArgTyIleValHisLeuGlnHisAsnLeuGlnLysGluGlu 60  
Db 305 CACTCGCTCAAGCCCGCTTACATGTTCACTTGGGGCAGCACCACTCCGAAGAGGAG 364  
Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 365 GGCTGTGAGCAGACCCGACGACCTGAGTCTTCCCCACCCTCCGCTTCAACAACAGC 424  
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 425 CTCGCCAACAAAGACCCGCAATGACATCATGTGTGAAGATGGCATCGCCAGTCTCC 484  
Qy 101 IleThrTpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 485 ATCACTGGGCTGTGGACCCCTCACCTCTCTCACTGCTGTGCTGTGCTGTGCTGTG 544  
Qy 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
Db 545 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCCAGTTACGCTCTCCCTCAC 604  
Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyProGlyAsn 160  
Db 605 CGATCGGCGCAACATCACCATTCATTGAGCACCAGAGTGTGAGAACGCTACCCCGGCA 664  
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
Db 665 ATCACAGACACCATGGTGTGTGCCAGCGTCCAGGAGGGGGCAAGGACTCTCTCCAG 724  
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200  
Db 725 GACTCCGGGGGCGCTCTGTGCTGTAAACAGTCTCTTCAAGGCATTATCTCTGGGGCC 784  
Qy 201 AspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyValAsp 220  
Db 785 GATCCGTTGCGATCACCCGAAAGCCTGGTGTCTACAGGAAGTCTGCAATATGTGGAC 844  
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229  
Db 845 TGGATCCAGGAGACGATGAAGACAAT 871

RESULT 7  
AB012174  
LOCUS AR152174 1192 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 8 from patent US 6232456.  
ACCESSION AR152174  
VERSION AR152174.1 GI:15118224  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1192)  
Cohen M., Colpitts T.L., Friedman P.N., Granados E., Klass M.R.,  
Russell J.C., Stewart K.D. and Stroupe S.D.  
Serrine protease reagents and methods useful for detecting and

JOURNAL  
 FEATURES  
 source  
 treating diseases of the prostate  
 Patent: US 6232456-A 8 15-MAY-2001;  
 Location/Qualifiers  
 1. 1192  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
 Pred. No.: 4.88e-97 Length: 1192  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AR152174 (1-1192)

Qy 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 170 ATCATCAAGGGGTCGAGTGCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 229  
 Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 230 AAGACGGCGTACTCTGTGGGGGACGCTCATGCCCGCCAGTGGCTCTTCGACGAGCC 289  
 Qy 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 Db 290 CACTGCTCAAGCCCGCTCATATGTTCACTGGGGCAGCACAACTCCAGAGGAGGAG 349  
 Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 350 GGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTTCCCGCCAGCTTCAACACAGC 409  
 Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 410 CTCCCGCAACAAAGACCCGACATGACATCATGCTGTGAGATGGATGCCAGTCTCC 469  
 Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 470 ATCACTGGGCTGTGCGACCCCTCACCTCTCTCTCAAGCTGTCTCACTGTGCGACCC 529  
 Qy 121 CysLeuLysSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 530 TGCTCTATTTCCGGCTGGGCGAGCAGCTCCAGCCCCAGTTACGCTGCTCTCACCTTG 589  
 Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
 Db 590 CGATGCGCAACATCACTATTCAGCAGCAGCAGAGTGTGAGAACGCTTACCCCGGCAAC 649  
 Qy 161 IleThrAspThrMetValCysAlaSerValClnclGlyGlyLysAspSerCysGlnGly 180  
 Db 650 ATCAGACACCATCGTGTGCGCAGCGTGCAGAGGGGCGAGGACTCTCTCCAGGGT 709  
 Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 710 GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCAATTATCTCTGGGGCCAG 769  
 Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpValAsp 220  
 Db 770 GATCCGTGTGCGATCACCCGAAAGCCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 829  
 Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229  
 Db 830 TGGATCCAGGAGACGATGAGAACAT 856

RESULT 8  
 AX358932  
 LOCUS AX358932 1204 bp DNA linear PAT 13-FEB-2002  
 DEFINITION Sequence 185 from Patent WO0193983.  
 ACCESSION AX358932  
 VERSION AX358932.1 GI:18675367  
 KEYWORDS

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Stephan,J.P.,  
 Godowski,P.J., Grimaldi,J.C., Gurrey,A.L., Smith,V., Watanabe,C.K. and Wood,W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0193983-A 185 13-DEC-2001;  
 Genentech Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 1204  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
 Pred. No.: 4.93e-97 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AX358932 (1-1204)

Qy 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
 Db 169 ATCATCAAGGGGTCGAGTGCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 228  
 Qy 21 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 229 AAGACGGCGTACTCTGTGGGGGACGCTCATGCCCGCCAGTGGCTCTTCGACGAGCC 288  
 Qy 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 Db 289 CACTGCTCAAGCCCGCTCATATGTTCACTGGGGCAGCACAACTCCAGAGGAGGAG 348  
 Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
 Db 349 GGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTTCCCGCCAGCTTCAACACAGC 408  
 Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCGCAACAAAGACCCGACATGACATCATGCTGTGAGATGGATGCCAGTCTCC 468  
 Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGCTGTGCGACCCCTCACCTCTCTCTCACGCTGTCTCACTGTGGACCCAGC 528  
 Qy 121 CysLeuLysSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCTCTATTTCCGGCTGGGCGAGCAGCTCCAGCCCCAGTTACGCTGCTCTCACCTTG 588  
 Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
 Db 589 CGATGCGCAACATCACTATTCAGCAGCAGCAGAGTGTGAGAACGCTTACCCCGGCAAC 648  
 Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180  
 Db 649 ATCAGACACCATCGTGTGTGCCAGCGTGCAGAGGGGCGCAAGGACTCTCTGGCAGGGT 708  
 Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCAATTATCTCTGGGGCCAG 768  
 Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpValAsp 220  
 Db 769 GATCCGTGTGCGATCACCCGAAAGCCCTGGTGTCTACAGAAAGTGTGCAAAATATGTGGAC 828

Qy	221	TripIeGlnGluThrMetLysAsn	229
Db	829	TGGATCCAGGACGATGAACAACAAAT	855
RESULT 9			
AX362425			
LOCUS	AX362425	1204 bp DNA linear	PAT 15-FEB-2000
DEFINITION	Sequence 185 from Patent WO0208288.		
ACCESSION	AX362425		
VERSION	AX362425.1	GI:18694670	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,		
	Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,		
	Watanabe,C.K. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
JOURNAL	the same		
FEATURES	Patent: WO 0208288-A 185 31-JAN-2002;		
source	Genentech, Inc. (US)		
	Location/Qualifiers		
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ORIGIN	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
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Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-856-320A-2_COPY_54_282 (1-229) x AX362425 (1-1204)			
Qy	1	IleIleLysGlyPheGluCysIysProHisSerGlnProTrpGlnAlaIleuPheGlu	20
Db	169	ATCATCAAGGGTTGCAGTGAAGCTCACATCCAGGCCCTGGCAGGCGCCGTTCGAG	228
Qy	21	LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla	40
Db	229	AAGACGCGCTACTCTGTGGGCGACGCTATCGCCCCAGATGGCTCCTGCACGACGCC	288
Qy	41	HisCysLeuLysProArgTyrlleValHisIeuGlyGlnHisasnIeuGlnIysGluGlu	60
Db	289	CACCTGGCTCAAGCCCGGTACATAGTTACCCTGGGCGACACAACTCCAGAGGAGGAG	348
Qy	61	GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer	80
Db	349	GGCTGTGACACACCCGGACACGCCACTGAGTCCTTCCCACCCCGGCTTCAACACACG	408
Qy	81	LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
Db	409	CTCCCCAACAAAGACACCGCAATGACATCATGTCTGTAAGATGGCATGGCCAGTCTCC	468
Qy	101	IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Db	469	ATCACCTGGGCTGTGCGACCCCTCACCTCTTCTACGCTGTGTCACTGCTGGCACCAGC	528
Qy	121	CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
Db	529	TGCCTCAITTCGGCTGGGGCGACGATCCAGCCCCAGTTACGCTGCTCACACCTTG	588
Qy	141	ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn	160
Db	589	CGATGGCCCAACATCACCATCATTAGACACACAGAAGTGTGAGAACGCCCTACCCCGCAC	648
Qy	161	IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly	180

```

QY      81  LeuProAsnIysAspHisArgAsnAspIleMetLeuValIysMetAlaSerProValSer 100
Db      409 CTCCCAACAAAGACCAACCGCATGACATCATGCTGCTGAAGATGGCATCGCAGTCTCC 468

QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469 ATCACCTGGCTGTGGCGACCCCTCACCTCTCTCTCACGCTGTGTCTACTCTGGCACCAGC 528

QY      121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db      529 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTACGCTGCTCACACCTTG 588

QY      141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db      589 CGATGCCCAACATCATCCATCATTTAGCACCAGACCAAGTGTGAGAACGCTTACCCCGCAAC 648

QY      161 IleThrAspThrMetValCysAlaSerValGlnGluGlyCysAspSerCysGlnGly 180
Db      649 ATCACAGACACCATGCTGTGTGTCAGCGTGCAGAAAGGGGGCAGACCTCTGCCAGGCT 708

QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGln 200
Db      709 GATCCCGGGGGCCCTCTGGTCTGTACCATGCTCTTCAAGGCATTTATCTCTGGGGCCAG 768

QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrIysValCysLysTyrValAsp 220
Db      769 GATCCGCTGTCGATCACCCGAAAGCCTGTGTCTACACGAAAGTCTGCAATATGTGGAC 828

QY      221 TrpIleGlnGluThrMetLysAsnAsn 229
Db      829 TGGATCCAGGAGCATGAAGACAAT 855

RESULT 11
AX464372 1204 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 505 from Patent WO0140466.
ACCESSION AX464372
VERSION AX464372.1 GI:21899202
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 505 07-JUN-2001;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Db      169 ATCATCAAGGGTTCAGTGCAGACCTTCACTCCAGCCCTGGCAGCGCCTGTTCGAG 228

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QY      21  LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
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QY      41  HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db      289 CACTGCTCTAAGCCCGCTACATAGTTCACTTGGGGCAGCACAACCTCCAGAAAGGGAG 348

QY      61  GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
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QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGln 200
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QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrIysValCysLysTyrValAsp 220
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LOCUS
DEFINITION Sequence 207 from Patent WO0200690.
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
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Db 289 CACTGCTCAAGCCCGCTACATAGTTTCACTGGGGCAGCACAACCTCCAGAGGAGGAG 348
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QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 769 GATCCGTGTGCGATCACCCGAAAGCGTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828
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RESULT 13
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DEFINITION Sequence 169 from Patent WO0078961.
ACCESSION AX697101
VERSION AX697101.1 GI:29498066
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ferrara N., Stewart T.A., Williams P.M., Baker K.P., Desnoyers L.,
Eaton D.L., Gao W.Q., Pan J., Botstein D., Fong S., Goddard A.,
Godowski P.J., Gurney A.L., Smith V., Tamas D., Wood W.I.,
Grimaldi C.J., Hillan K.J., Paoni N.F., Roy M.A. and Watanabe C.K.
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ACCESSION AY359014  
VERSION AY359014.1 GI:37183145  
KEYWORDS FLI\_CDNA  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1204)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
JOURNAL Genom Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 1204)  
AUTHORS Clark,H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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VERSION BC022068.1 GI:18314497  
KEYWORDS MGC.  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1213)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
Diatchenko,L., Narusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvachenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,  
Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
JOURNAL MEDLINE 22388257  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 1213)  
AUTHORS Strausberg,R.  
TITLE Direct Submission



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: June 23, 2004, 01:23:08 ; Search time 88 Seconds

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1444.134 Million cell updates/sec

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Maximum Match 100%

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4	1248	99.2	1146	4	US-09-205-258-247
5	1246	99.0	1166	3	US-08-944-483-7
6	1219.5	96.9	1052	4	US-09-386-642-10
7	1213	96.4	833	2	US-08-790-137-2
8	916.5	72.9	618	4	US-09-280-116-3
9	681	54.1	944	3	US-09-070-526-1
10	681	54.1	1343	4	US-09-618-259-72
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#### ALIGNMENTS

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US-08-944-483-8

; Sequence No. 6232456

; Patent No. 6232456

; GENERAL INFORMATION:

; APPLICANT: COHEN, MAURICE

; APPLICANT: COLFITS, TRACEY L.

; APPLICANT: FRIEDMAN, PAULA N.

; APPLICANT: GRANADOS, EDWARD N.

; APPLICANT: KLASS, MICHAEL R.

; APPLICANT: RUSSELL, JOHN C.

; APPLICANT: STEWART, KENT D.

; APPLICANT: STROUPE, STEVEN D.

; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/944,483

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 8:
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Alignment Scores:
Pred. No.: 7,33e-125 Length: 1192
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-944-483-8 (1-1192)

Qy 1 IleIleIleGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20
Db 170 ATCATCAAGGGGTCGAGTCGAGCCCTCACTCCAGCCCTGGCAGCAGCCCTGTTTCGAG 229

Qy 21 LysThrArgLeuLeuGlyCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
Db 230 AAGACGGCGTACTCTGTGGGCGAGCGCTCATGCCGCCAGATGCTCTCTGACAGCAGCC 289

Qy 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnGlu 60
Db 290 CACTGCTCAAGCCCGCTCATAGTTACCTGGGCGAGCAGCAACCTCAGAGGAGGAG 349

Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db 350 GGCTGTGAGCAGACCCCGCAGCAGCAGTACTGCTTCCCCACCCCGGCTTCACACACAGC 409

Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 410 CTCCCCAACAAAGACCAACCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 469

Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 470 ATCACTGGGCTGGGCGAGCAGCAGTACCTCTCTCAGCTGTGTCTCTGCTGCGACACAGC 529

Qy 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 530 TGCCTCATTTCCGGCTGGGCGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCTCACACCTTG 589

Qy 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 590 CGATGCCGCCAACATCACCATTGAGCAGCAGAGGTGAGAACGCTTACCCCGGCAAC 649

Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 650 ATCACACACACCATGTTGTGTGCGAGGTGCGAGAGGGGGCAGGACTCTCTCCAGGCT 709

Qy 181 AspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 710 GACTCCGGGGCCCTCTGCTGTGTAACAGCTCTTCAAGGCATTATCTCTGGGGCCAG 769

Qy 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 770 GATCCGTGCGGATCACCCGAGGCTGGTGTCTACACGAACTCTGCAATATGTGGAC 829

Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229

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Db 830 TGGATCCAGGAGACCATGATCAAGACCAAT 856

RESULT 2

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US-09-205-358-189
; Sequence 189, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883

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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 189  
LENGTH: 1292  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-205-258-189

Alignment Scores:  
Pred. No.: 8,27e-125 Length: 1292  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-205-258-189 (1-1292)

QY 1 IlellelyGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
DB 270 ATCATCAGGGTTCAGTGTGAGGCTCTACCTCCAGCCCTGCAGCAGCCCTGTTCGAG 329

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuAlaAla 40  
DB 330 AAGACGGCGTACTCTGTGGGGAGCGCTCATCGCCCGCCAGATGGCTCTGACAGCAGCC 389

QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
DB 390 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCAACCTCCAGAGGAGGAG 449

QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 450 GGCTGTGAGCAGACCCGGACAGCCTAGTCTTCCCGCCCGGCTTCAACACAGC 509

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 510 CTCCTCCCAACAAAGACACCGCATGATGATCATGCTGTGTGAAGTGCATCGCAGTCTCC 569

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 570 ATCACTGGGTGTGGAGCCCTCACCTCTCTACGCTGTCTACTGCTGGCACCAGC 529

QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
DB 630 TGYCTCATTTCCGGCTGGGGCAGCAGCTCAGCCCGCCAGTACGCTGCTCACACCTTG 689

QY 141 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
DB 690 CGATGGCCCAACATCACCATCATTTGAGCACCAGAGTGTGAGAACCCCTACCCCGGCAAC 749

QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180  
DB 750 ATCAGACACCATGTTGTGTGTCAGCGTGCAGGAAGGGGCAAGGACTCTCTGCCAGGCT 809

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIlelleSerTrpGlyGln 200  
DB 810 GACTCCGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTGGGGCCAG 869

QY 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220  
DB 870 GATCCGTGTGGATCATCCCGAAAGCCCTGGTGTCTACACGAAAGTCTCAAAATATGTGAC 929

QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
DB 930 TGGATCCAGGAGACGATGAAGAACAT 956

RESULT 3  
US-09-025-059-2  
Sequence 2, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGTUT10  
CLONE: 2723646  
US-09-025-059-2

Alignment Scores:  
Pred. No.: 8,49e-125 Length: 1314  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-025-059-2 (1-1314)

QY 1 IlellelyGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
DB 287 ATCATCAGGGTTCAGTGTGAGGCTCTACCTCCAGCCCTGCAGCAGCCCTCTTCGAG 346

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Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
Db 347 AAGAGCGGGCTACTCTGTGGGGGAGCGCTCATCGCCGCCAGATGGCTCTGACAGAGCC 406
Qy 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnGluGlu 60
Db 407 CACTGCCTCAAGCCCGCTACATAGTTCACTCGGGCAGCACCACTCCAGAGGAGGAG 466
Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGluPheAsnAsnSer 80
Db 467 GGCTGTGAGCAGACCCGAGCAGCAGTGAAGTCTTCCGCCACCCCGGCTTCACACACG 526
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 527 CTCCCAACCAAGACCAACCCGATGATGATGATGATGATGATGATGATGATGATGATG 586
Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 587 ATCACTGGGCTGTGGGACCCCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 646
Qy 121 CysLeuLeuSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140
Db 647 TGCTCTATTTCCGGTGGGCGAGCAGCTCCAGCCCGGCTTACGCTGCTCTCACACCTTG 706
Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
Db 707 CGATGCCCAACATCACTCATGTAGCAGCAGAGTGAGAACGCTTACCCCGGCAAC 766
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyCysLysAspSerCysGlnGly 180
Db 767 ATCACAGACACCATGGTGTGTGCGAGCGTGCAGAGGGGGGCAAGACTCTCTGCCAGGT 826
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 827 GACTCCGGGGGCGCTCTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 886
Qy 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysValValAsp 220
Db 887 GATCCGTTGCGATCACCAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 946
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 947 TGGATCCAGGAGCAGATGAAGAACAT 973

RESULT 4
US-09-205-258-247
; Sequence 247, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 247
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
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; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: n equals a.t.g, or c
; US-09-205-258-247

Alignment Scores:
Pred. No.:      8 07e-124      Length:      1146
Score:          1248.00      Matches:      227
Percent Similarity: 99.13%      Conservative: 0
Best Local Similarity: 99.13%      Mismatches: 2
Query Match:     99.21%      Indels:      0
DB:              4          Gaps:      0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-205-258-247 (1-1146)
QY 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 124 ATCATCAAGGGTTCAGAGTCAAGCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCGAG 183
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 184 AAGACGGGTACTCTCTGTGGGGCAGCGCTCATCGCCCGCAGATGGCTCTGACGAGCC 243
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 244 CACTGGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACACCTCCAGAAGGAGGAG 303
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
Db 304 GGCTGTGAGCAGACCCGGGAGCAGCAGTGTCTTCCCCCACCCTGGCTTCAACACAGC 363
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 364 CTCCCAACAAAGACCCAGCATGATCATCTGTGTAAGTGCATCGCCAGCTCC 423
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 424 ATCACTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTCTACTGTCGACGACG 483
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 484 TGYCTCATTTCCGGCTGGGGCAGMACGTCCAGCCCCAGTTACGCTGCTCACACTTG 543
QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 544 SGATGCCCAACATCAACATCAATTGAGCAGCAGAGTGTGAGAAGCGCTACCCCGCAAC 603
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluClyGlyLysAspSerCysGlnGly 180
Db 604 ATCACACACCACTGGTGTGGCAGCGTGCAGAGGGGGCAGGACTCTCTCCAGGGT 663
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200
Db 664 GACTCCGGGGCCCTCTGGTCTGTGACCACTCTTCAAGGCATTATCTCTCTGGGCGCAG 723
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 724 GATCCGTGTGGATCACCCGAAAGCCCTGGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 783
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 784 TGGATCCAGGAGACATGAGAAACAAT 810

RESULT 5
US-08-944-483-7
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; Sequence 7, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-944-483-7

Alignment Scores:
Pred. No.:      1,35e-123      Length:      1166
Score:          1246.00      Matches:      227
Percent Similarity: 99.13%      Conservative: 0
Best Local Similarity: 99.13%      Mismatches: 2
Query Match:     99.05%      Indels:      0
DB:              3          Gaps:      0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-944-483-7 (1-1166)
QY 1 IleileLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 166 ATCATCAAGGGTTCAGAGTCAAGCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCGAG 225
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 40
Db 226 AARACGGGCTACTCTGTGGGGCAGCGTTCATCGCCCGCAGATGGCTCTGACAGCAGCC 285
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
Db 286 CACTGGCTCAAGCCCGCTACATAGTTCACTCTGGGGCAGCACACCTCCAGAAGGAGGAG 345
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
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Db 346 GGCTGTGAGCAGACCCGACGACGCTGAGTCTTCCCCCACCCTCCGCTTCAACAACAGC 405  
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 406 CTCCCCAACAAAGACCCGCAATGACATCATGCTGTGAAGATGGCATCGCCAGTCTCC 465  
Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 466 ATCACTCTGGGTGTGGCAGCCCTCACCCTCTCTCTCAAGCTGTGTCACTGTGTCACCCAGC 525  
Qy 121 CysLeuIleSerGlyTTPGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
Db 526 TGCTCTCAITTCGGCTGGGCGAGCAGCTCCAGCCCCCAGTTAGCTGTGCTCACACTTG 585  
Qy 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 586 CGATGCGCCCAACATCAACCATATTGAGCAGCAGAGGTGTGAGAACGCTTACCCCGGCAAC 645  
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180  
Db 646 ATCAACAGACCATGTGTGTGCGCAGCTGTGCGAGAGGGGCGAGGACTCTCTGCCAGGGT 705  
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 200  
Db 706 GACTCCGGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAAGGCATTATCTCTCGGGCCAG 765  
Qy 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
Db 766 GATCCGTGTGGATCAACCCGAAAGCCGTGTGTACACGAAAGTGTGCAAAATATGTGGAC 825  
Qy 221 TriPleGlnGluThrMetLysAsnAsn 229  
Db 826 TGGATCCAGGAGACGATGAAGAACAT 852

## RESULT 6

US-09-386-642-10  
; Sequence 10, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1052  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-10

## Alignment Scores:

Pred. No.:	7,84e-121	Length:	1052
Score:	1219.50	Matches:	223
Percent Similarity:	98.26%	Conservative:	3
Best Local Similarity:	96.96%	Mismatches:	1
Query Match:	96.94%	Indels:	4
DB:	4	Gaps:	1

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-386-642-10 (1-1052)

Qy 1 IleIleLysGlyPheGluCys---LysProHisSerGlnProTrpGlnAlaLeuPhe 19  
Db 166 ATGTTGGGGGCTACCAACTGTCTAGAAAGCATCCAGCCCTGGCAGGACGCCCTGTTC 225  
Qy 20 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 39

Db 226 GAGAAGACCGGCTACTCTGTGGGCGAGCGCTATCGCCCCCAGATGGCTCTCCACAGCA 285  
Qy 40 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 59  
Db 286 GCCCACTCGCTCAAGCCCGCTACATAGTTCCCTGGGGCAGCACAACTCCAGAGGAG 345  
Qy 60 GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 79  
Db 346 GAGGGCTGTGAGCAGACCCGACAGCCACTGAGTCTCTTCCCCCACCCTCCGCTTCAACAAC 405  
Qy 80 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 99  
Db 406 AGCTCTCCCAACAAAGACACCGCAATGACATCATGTGGTGAAGATGGCATCGCCAGTC 465  
Qy 100 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 119  
Db 466 TCCATCACTGGGCTGTGCGACCCCTCACCTCTCTCTCACGCTGTGTCACTGTGGCACC 525  
Qy 120 SerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThr 139  
Db 526 AGCTCCCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCCCAGTTACGGCTGCTCACACC 585  
Qy 140 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 159  
Db 586 TGGCATCGGCCAACATCACCATATTGAGCAGCAGCAAGTGTGAGAACGCTTACCCGGC 645  
Qy 160 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGln 179  
Db 646 AACATCAAGACACCATGTGTGCGCAGCGTGTGAGGAGGGGCGAGGACTCTCTGCCAG 705  
Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199  
Db 706 GGTGACTCCGGGGGCCCTCTGTCTGTAAACCAGTCTCTTCAAGGCATTATCTCTCTGGGC 765  
Qy 200 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 219  
Db 766 CAGGATCCGTGTGCGATCACCCGAAAGCCGTGTCTTACACGAAAGTCTGCAATATGTG 825  
Qy 220 AspTriPleGlnGluThrMetLysAsnAsn 229  
Db 826 GACTGTGATCCAGGAGACGATGAAGAACAT 855

## RESULT 7

US-08-790-137-2  
; Sequence 2, Application US/08790137  
; Patent No. 5840871  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Goli, Surya K.  
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED  
; TITLE OF INVENTION: KALLIKREIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/790,137  
; FILING DATE: Filed Herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-835-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-790-137-2

Alignment Scores:
Pred. No.: 2,728-120 Length: 833
Score: 1213.00 Matches: 219
Percent Similarity: 97.82% Conservative: 5
Best Local Similarity: 95.63% Mismatches: 5
Query Match: 96.42% Indels: 0
DB: Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-08-790-137-2 (1-833)
QY 1 IIEIIELYSGLYPHEGLUCYLSYSPROHISERGLNPROTRPGINLALALALEUPHEGLU 20
DB 99 ATTGTGGAGGCTGGAGGTGTGAGCAGCATCCAGCCCTGGCAGCGCTCTGTACCAG 158
QY 21 LYSTHRARGLEULEUCYSGLYALATHRLEULIEALAPROARGTRIPLEULEUTHRALALA 40
DB 159 AAGACGCGGCTACTCTGTGGGCGCAGNFCATNGCCCCAGATGTTCTTGACACAGCC 218
QY 41 HISCYSLVLEUPROARGTYRILEVALHISLEUGLYGLNHISASNLEUGLNYSGLUGLU 60
DB 219 CACTGCTNAAGCCCGCTACATAGTTTCACTGGGGCAGCACAACTCCAGAAAGGAGG 278
QY 61 GLYCYSGLUINLTHRARGTHRALATHRGLUSERPHEPROHISERPROGLYPHEASNANSEN 80
DB 279 GGTGTGACGACAGCCGCGACGCACTGAGTCTCTCCGCCACCCCGGCTTCAACACAGC 338
QY 81 LEUPROASNLYASPHISARGASNAPILEMETLEUVALLYSMETALASERPROVALSER 100
DB 339 CTCGCCCAACAGACACCCGCAATGACATCATGTGTTGATGGATCGCATCGCCATCCC 398
QY 101 ILETTRTPALAVARGPROLEUTHRLEUSERSERARGCYSAVALTHRALAGLYTHRSE 120
DB 399 ATCACCTGGGCTGTGGACCCCTCACCTCTCTCAGCGTGTGTCACTGCTGGCACCAGC 458
QY 121 CYSEULEISERGLYTRPGLYSERTHRSESRPROGLINLEUARGLEUPROHISLTHRLEU 140
DB 459 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTACGCTGCTCTCACCTTG 518
QY 141 ARGCYSAALASNILETHRILEGLUHIHISGLNLYSYSGLUASNALATYRPROGLYASN 160
DB 519 CGATGCCCAACATCACCATCATTTGAGCACCAGAGTGTGAGAACGCTTACCCCGCAAC 578
QY 161 ILETTRASPTHRMETVALCYSAASERVALGLNGLUGLYGLYLSASPSERCYSGINGLY 180
DB 579 ATCACAGACACCATGTTGTGTGTCAGCGTGCAGGAAGGGGCAAGGACCTCTGCCAGGT 638
QY 181 ASPSERGLYGLYPROLEUVALCYASNGLNSERLEUGLNGLYILEILESERTRPGLYGLN 200
DB 639 GATCTCGGGGGCCCTCTGTGTTGTATACCAAGTCTCTTCAGAGGCATATCTCTCTGGG 698
QY 201 ASPPROCYSAALALETHRARGLYSPROGLYVALTYRTHLYSVALCYSLYSTYRVALASP 220
DB 699 GATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 758
QY 221 TRPILGLNGLUHRMETLYSASNAN 229
DB 759 TGGATCCAGGAGCAGATGAAGAACAT 785

RESULT 8
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```
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3

Alignment Scores:
Pred. No.: 7,978-89 Length: 618
Score: 916.50 Matches: 184
Percent Similarity: 90.78% Conservative: 3
Best Local Similarity: 89.32% Mismatches: 4
Query Match: 72.85% Indels: 16
DB: Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-280-116-3 (1-618)
QY 23 ARGLEULEUCYSGLYALATHRLEULIEALAPRO-ARGTRIPLEULEUTHRALALAHISCY 42
DB 2 CGGTACTCTGTGGGGGACCC---TCATCGCTCTAGATGGCTCTGTGACAGAGCCCACTG 58
QY 42 SLEULYSPROARGTYRILEVALHISLEUGLYGLNHISASNLEUGLNYSGLUGLYCY 62
DB 59 CCTCAAGCCCGCTTACATAGTTTCACTGGGGCAGCACAACTCCAGAAAGGAGGAGGCTG 118
QY 62 SGLUGLNTHRARGTHRALATHRGLUSERPHEPROHISERPROGLYPHEASNANSENLEUPR 82
DB 119 TGACGACAGCCGCGACGCCACTGAGTCTTCCGCCACCCCGGCTTCAACACAGCCCTCC 178
QY 82 OASNLYASPHISARGASNAPILEMETLEUVALLYSMETALASERPROVAL-SERILET 102
DB 179 CAACAAGACCAACCGCATGACATCATGTGTTGATGGATGGCATGGCTGCCATCA 238
QY 102 HRTPALAVARGPROLEUTHRLEUSERSERARGCYSAVALTHRALAGLYTHRSECYSL 122
DB 239 CCTGGGCTGTGGACCCCTCACCTCTCTCATGCTGTGTCTGTGCTGGCACCAGCTGCC 298
QY 122 EULEISERGLYTRPGLYSERTHRSESRPROGLINLEUARGLEUPROHISLTHRLEUARGC 142
DB 299 TCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTACGCTGCTCTCACCTTGGAT 358
QY 142 YSALAASNILETHRILEGLUHIHISGLNLYSYSGLUASNALATYRPROGLYASNILET 162
DB 359 CGGCCAACATCACCATCATTTGAGCACCAGAGTGTGAGAACGCTTACCCCGCAACATCA 418
QY 162 HRASPTHRMETVALCYSAASERVALGLNGLUGLYGLYLSASPSERCYSGINGLYASPS 182
DB 419 CAGACACCATGTTGTGTCAGCGTGAAGGAGGGGCAAGGACTCTTCCCA----- 471
QY 182 ERGLYGLYPROLEUVALCYASNGLNSERLEUGLNGLYILEILESERTRP-GLYGLNASP 201
DB 472 -----GTCTCTTC-AAAGGCATTTATCTCTGGGGGCGCAGGAC 507
QY 202 -PROCYSAALALETHRARGLYSPROGLYVALTYRTHLYSVALCYSLYSTYRVALASPTR 221
DB 508 TCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAGAAAGTCTGCAAAATATGTGGACTG 567
QY 221 TRPILGLNGLU 224
DB 568 GATCCAGGAA 577
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QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 612 CACTGTAAAAAACCAGAAATACACAGTACGCTGGGAGACACACAGCCTACAGAAATAAGAT 553  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 552 GGCCAGAGCAAGAAATACCTGTGTTGATGCTCATCCACACCCCTGTACAAACAGCAGC 493  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 492 ---GATGTGGAGGAGCACCAACCATGATCTGATCTTCTCACTGGGTGACCGCATCC 436  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 435 CTGGGGTCCAAAGTGAAGCCCATCAGCTGGCAGATCATTCACCCAGCCTGGCCAGAG 376  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
Db 375 TGACCGCTCTCAGCTGGGGCACTGTCCACAGTCCCGGAGAAATTTCTGACACTCTC 316  
QY 141 ArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 315 AACTGTGCAGAGTAAATAATCTTCCAGAGAAAGTGTGAGGATGCTTACCCGGGGCAG 256  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180  
Db 255 ATCAGAGTGGCAGTGTCTGTGCGAGCAGCAGCAAGGGGCT---GACACGTGCCAGGC 199  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 198 GATTCGTGGAGGCCCTGGTGTGTGATGTGTCACCTCCAGGCATCATCTCTGGGGCTCA 139  
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220  
Db 138 GACCCCTGTGGGAGTCCAGAAACCTGGCGTCTATACCAACATCTCGCGCTACCTGGAC 79  
QY 221 TrpIleGlnGlu 224  
Db 78 TGGATCAAGAAG 67

## RESULT 11

US-09-618-259-6  
; Sequence 6, Application US/09618259  
; Patent No. 6642013  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Underwood, Lowell J.  
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
; FILE REFERENCE: D6020CIP2  
; CURRENT APPLICATION NUMBER: US/09/618,259  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: US 09/127,444  
; PRIOR FILING DATE: 1998-08-21  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 6  
; LENGTH: 1360  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence encoding Tumor Antigen Derived  
; OTHER INFORMATION: Gene-14 (TAGD-14) protein; nt 1344-1360 NCBI accession  
; OTHER INFORMATION: #AA343629  
US-09-618-259-6

Alignment Scores:  
Pred. No.: 3,69e-63 Length: 1360  
Score: 681.00 Matches: 116  
Percent Similarity: 70.54% Conservative: 42  
Best Local Similarity: 51.79% Mismatches: 64  
Query Match: 54.13% Indels: 2  
DB: 4 Gaps: 2

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-618-259-6 (1-1360)

QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
Db 612 GTGCTGGGGGTCTCATGAGTGCACCAACCCCATTCGCGAGCCTTGGCAGCGGCTTGTTCAG 671  
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
Db 672 GGCCAGCAACTACTCTGTGGCGGTGCTCTTGTAGTGGCAACTGGGTCTTACAGCTGCC 731  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 732 CACTGTAAAAAACCAGAAATACACAGTACGCTGGGAGACACACAGCCTACAGAAATAAGAT 791  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 792 GGCCAGAGCAAGAAATACCTGTGTTGATGCTCATCCACACCCCTGTACAAACAGCAGC 851  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 852 ---GATGTGGAGGAGCACCAACCATGATCTTCTCACTGGGTGACCGCATCC 908  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 909 CTGGGGTCCAAAGTGAAGCCCATCAGCTGGCAGATCATTCACCCAGCCTGGCCAGAG 968  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 140  
Db 969 TGCACCTCTCAGCTGGGGCACTGTCCACAGTCCCGGAGAGAAATTTCTGACACTCTC 1028  
QY 141 ArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 1029 AACTGTGCAGAGTAAATAATCTTCCAGAGAAAGTGTGAGGATGCTTACCCGGGGCAG 1088  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180  
Db 1089 ATCAGAGTGCATGCTGTGTGCGAGCAGCAGCAAGGGGCT---GACACGTGCCAGGC 1145  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 1146 GATTCGTGGAGGCCCTGGTGTGTGATGTGTCACCTCCAGGCATCATCTCTGGGGCTCA 1205  
QY 201 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAsp 220  
Db 1206 GACCCCTGTGGAGTCCGCAACACCTGGGTCTATACCAACATCTCGCGCTACCTGGAC 1265  
QY 221 TrpIleGlnGlu 224  
Db 1266 TGGATCAAGAAG 1277

RESULT 12  
US-09-008-271A-19  
; Sequence 19, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible



QY 140 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGly 159  
 Db 583 CTCACACTGTGCAGAAATAATCTTTCCACAGAGAGTGTGAGGATCTTACCGGGG 642  
 QY 160 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGln 179  
 Db 643 CAGATCACAGATGGCATGTCTGTGAGGAGCAGCAAAAGGGGCT---GACACGTGCCAG 699  
 QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199  
 Db 700 GCGGATCTGGAGGCCCTGGTGTGTGATGTGCTACCCAGGATCATCATCTGGGGC 759  
 QY 200 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 219  
 Db 760 TCAGACCCCTGTGGGAGTCCGACAAACCTGGCTATATACCAACATCTGCCGCTACCTG 819  
 QY 220 AspTrpIleGlnGlu 224  
 Db 820 GACTGGATCAAGAG 834

## RESULT 14

US-09-509-908-1  
 ; Sequence 1, Application US/09509908  
 ; Patent No. 6589770  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company, N/A N/A  
 ; TITLE OF INVENTION: A Protease  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: T. David Reed  
 ; STREET: 5299 Spring Grove Avenue  
 ; CITY: Cincinnati  
 ; STATE: Ohio  
 ; COUNTRY: USA  
 ; ZIP: 45217-1087  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/509,908  
 ; FILING DATE: 28-Feb-2002  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Reed, T David  
 ; REGISTRATION NUMBER: 32,931  
 ; REFERENCE/DOCKET NUMBER: AA-264F  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 513-627-7025  
 ; TELEFAX: 513-627-6333  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1499 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 291..1172  
 ; FEATURE:  
 ; NAME/KEY: mat\_peptide  
 ; LOCATION: 489..1172  
 ; FEATURE:  
 ; NAME/KEY: 5'UTR  
 ; LOCATION: 1..290  
 ; FEATURE:  
 ; NAME/KEY: 3'UTR  
 ; LOCATION: 1173..1499  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-509-908-1

Alignment Scores:  
 Pred. No.: 3.38e-59 Length: 1499  
 Score: 644.50 Matches: 117  
 Percent Similarity: 67.97% Conservative: 40  
 Best Local Similarity: 50.55% Mismatches: 67  
 Query Match: 51.23% Indels: 7  
 DB: 4 Gaps: 4

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-509-908-1 (1-1499)

QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAa---LeuPhe 19  
 Db 489 ATCATCAATGATCCGACTGCGATATGCACACCGCGGTGGCAGCGCGCTGTCTCTA 548  
 QY 20 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAla 39  
 Db 549 AGGCCAACACAGCTCTACTGCGGGCGGTGTGTGTGCATCCACAGTGGTCTCACGGCC 608  
 QY 40 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys-- 58  
 Db 609 GCCCACTGCAGGAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCCACAGTT 668  
 QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78  
 Db 669 TATCAATCTGGCAGCAGATCTTCCAGGGGTCAATCCATCCCCACCTGGCTACTCC 728  
 QY 79 AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 98  
 Db 729 -----CACCTGGCCACTCTAAGACCTCATGTCTCAAACTGAACAGAGA 776  
 QY 99 ValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 118  
 Db 777 ATTCGTCCTAAAGATGTCAGACCCATCAAGCTCTCTCTCATTTGCTCTGCTGGG 836  
 QY 119 ThrSerCysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHis 138  
 Db 837 ACAAAGTCTGTGTCTGTGGTGGGGACAACAAGAGCCCCCAAGTGCACTTCCCTAAG 896  
 QY 139 ThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrPro 158  
 Db 897 GTCCTCCAGTCTTGAATATCAGCGTCTAAGTCAGAAAGGTGCGAGGATGCTTACCCG 956  
 QY 159 GlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCys 178  
 Db 957 AGACAGATAGATGACACCATGTTCTGCGCCGGT---GACAAAGCAGGTAGAGACTCTCGC 1013  
 QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 198  
 Db 1014 CAGGGTGATTCCTGGGGGCGCTGTGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCTCGG 1073  
 QY 199 GlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyr 218  
 Db 1074 GGAGATTACCTTGTGCGCGCCCAACAGACCGGGTGTCTACAGAACCTCTGCAAGTTC 1133  
 QY 219 ValAspTrpIleGlnGluThrMetLysAsnAsn 229  
 Db 1134 ACCAAGTGGATCCAGGAACCATCCAGGCCAAC 1166

## RESULT 15

US-09-280-116-20/c  
 ; Sequence 20, Application US/09280116A  
 ; Patent No. 6331427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
 ; FILE REFERENCE: 5800-24 035800/176965  
 ; CURRENT APPLICATION NUMBER: US/09/280,116A  
 ; CURRENT FILING DATE: 1999-03-26  
 ; NUMBER OF SEQ ID NOS: 268  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 1364  
 ; TYPE: DNA

Thu Jun 24 10:06:29 2004

Job time : 99 secs

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1364)
; OTHER INFORMATION: n = a, t, c, or g
US-09-280-116-20

Alignment Scores:
Pred. No.:      3.43e-58      Length:      1364
Score:          634.50      Matches:      123
Percent Similarity: 64.82%      Conservative: 41
Best Local Similarity: 48.62%      Mismatches: 60
Query Match:      50.44%      Indels:      29
DB:               4          Gaps:         3

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-280-116-20 (1-1364)

Qy      4  GlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArg 23
Db      828 GGCTACACCTGCTCCGCCACTCTCAGCCCTGCGAGCTGCCCTACTAGTGAAGGCGG 769

Qy      24  LeuLeuCysGlyAlaThr-LeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLe 43
Db      768 CTACTCTGTGGGGAAGTCTGTGTCACCCCAATGGTCTCTCACTGCCGCCACACTGTCT 709

Qy      43  uLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGl 63
Db      708 AAGGAGGGGCTCAAAATTACCTAGGCAAGCAGCCCTAGGGCGTGTGGAAGCTGGTGA 649

Qy      63  uGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAs 83
Db      648 GCAGGTGAGGGAAGTGTGTCACCTATCCGCCACCTGAAATACCGGAGAGGCCCCACCCA 589

Qy      83  nLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTr 103
Db      588 CTTGAACCAACNACCATGACATCATGCTTCTGGAGCTGCAGTCCCGGTCCAGCTCACAGG 529

Qy      103  pAlaValArgProLeuThrLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 122
Db      528 CTACATCCAAACCTGCGCTTCCCAACACACCCCTTAACCCCTGGCACCACCTGTGCG 469

Qy      122  uIleSerGlyTrpGlySerSerProGln-----LeuAr 135
Db      468 GGTGCTGGCTGGGGACCAACACCGCCCGGATGTCACCCACACAGGTGCTGAG 409

Qy      135  g-----Le 136
Db      408 GCCCATAGGAGTGGTGGGAAACACAGGCGAGATGGAGGGAAGTCTGAGTGAATT 349

Qy      136  uProHis-ThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnA 156
Db      348 ACCCAAAACTACATGTGCCAACAATCCAACTTCCTCAGATGAGGAGTGTGCTCAAG 289

Qy      156  laTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyIleA 176
Db      288 TCTACCCAGGAAGATCACTGACAAACATGTTGTGTCGGCGCAAAAGAGGGTGGCAAG 229

Qy      176  spSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIleI 196
Db      228 ACTCTGTGAGGTGACTCTGGGGGGCCCTGTGCTGTAAACAGAACACTGTATGGCATCG 169

Qy      196  leSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValC 216
Db      168 TCTCCTGGGAGACTTCCCATGTGGGCAACCTGACCGGCTGTGTCTACACCCGTGTCT 109

Qy      216  ysLysTyrValAspTrpIleGlnGluThrMetLys 227
Db      108 CAGATACGTCTGTGGATCCGTGAACAATCCGA 74

```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 23, 2004, 01:21:03 ; Search time 2957 Seconds  
(without alignments)  
2312.627 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258

Sequence: 1 IIKPCKPHSQPWAALPE.....GYTKVKYVDVIQETMKNN 229

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US09856320/runat\_22062004\_172806\_11879/app\_query.fasta\_1.391  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320@cgn\_1.1 6425 @runat\_22062004\_172806\_11879 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_rus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223.5	97.3	1282	11	BC015551 Homo sapi
2	1158	92.1	841	12	BI818697
3	1146	91.1	678	12	BI783040
4	1141	90.7	853	12	EG720793
5	1112.5	88.4	1072	12	BM559782
6	1062	84.4	1295	11	AK009360 Mus muscu
7	1062	84.4	1295	11	AK009720 Mus muscu
8	1061.5	84.4	1074	12	BM559617
9	1036	82.4	1269	11	AK009659
10	1008	80.1	753	29	AY410892 Homo sapi
11	992	78.9	556	29	AY410893
12	958	76.2	708	12	EG697071
13	895	71.1	592	14	CF768612
14	852	67.7	639	12	CG747134
15	834	66.3	556	29	AY410894
16	792.5	63.0	973	10	BE867930
17	780	62.0	761	12	BM982377
18	775	61.6	528	13	EX528424
19	744.5	59.2	747	13	EX109836
20	724	57.6	467	9	AI893370
21	720	57.2	467	9	AA073833
22	684	54.4	783	29	AY410900
23	684	54.4	880	14	CB202840
24	681	54.1	783	29	AY410898
25	678	53.9	898	14	CB204935
26	664	52.8	539	12	BM837078
27	664	52.8	852	14	CB587168
28	657	52.2	783	29	AY410899
29	639	50.8	826	14	CB574882
30	630	50.1	1048	11	AK004807
31	626	49.8	673	13	BU684799
32	623.5	49.6	1240	11	AK003996
33	620.5	49.3	368	9	AA412318
34	607	48.3	451	14	W60374
35	603	47.9	754	12	BI653899
36	598.5	47.6	965	13	BY709314
37	598	47.5	765	13	BU488441
38	597.5	47.5	890	11	AK009217
39	597	47.5	801	13	BU417451
40	595	47.3	766	13	BU416879
41	595	47.3	786	13	BU416290
42	595	47.3	793	13	BU487643
43	595	47.3	808	13	BU416510
44	595	47.3	810	13	BU417474
45	595	47.3	811	13	BU417330

# ALIGNMENTS

RESULT 1  
BC015551  
LOCUS BC015551 1282 bp mRNA linear HTC 17-DEC-2003  
DEFINITION Homo sapiens cDNA clone IMAGE:3847565, containing frame-shift errors.  
ACCESSION BC015551  
VERSION BC015551.2 GI:34190438  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1282)

AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bueckow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gundaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Kettaman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 1282)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> On Aug 25, 2003 this sequence version replaced gi:15930236. Contact: MGC help desk Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcdpaxil@stanford.edu">mcdpaxil@stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	source Location/Qualifiers 1..1282 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="NIH_MGC_65" /tissue_type="Colon, adenocarcinoma" /clone_lib="NIH_MGC_65" /lab_hosts="DH10B" /note="vector: pcwv-sport6"
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US-09-856-320A-2_COPY_54_282 (1-229) x BC015551 (1-1282)	
QY	1 llelellysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20 

Db	266	ATCATCAAGGGTTGAGTTCAGACCTCACTCCAGCCCTGGCAGCGCCCTGTTCAAG	325
QY	21	LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla	40
Db	326	AAGACGGGGTACTTGTGGGGGACGCTCATCGCCCAAGATGGCTCTCTGACAGCAGCC	385
QY	41	HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysG	59
Db	386	CACCTGCCTCAAGCGGTGGCGGCTACATAGTTCACTGGGGCAGCACAACCTCCAGAAGA	445
QY	59	uGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAs	79
Db	446	GGAGGGGTGTGACGACAGCCCGCAGCAGCATGTAGTCTCTCCCAACCCCGGCTTCAACA	505
QY	79	nSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVa	99
Db	506	CAGCCTCCCAACAAGACCAACCGCAATGACATCATCTGTTGAAGATGGCATCGCCAGT	565
QY	99	lSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyTh	119
Db	566	CTCCATCACCTGGGCTGTGGACCCCTCACCCCTCTCTCAGCTGTGTCTACTGCTGGCAC	625
QY	119	rSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisTh	139
Db	626	CAGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCAGTTACGCTGCTCACAC	685
QY	139	rLeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyProGl	159
Db	686	CTTCGATCGCCCAACATCCATCATTTGAGCAGCAGAGTGTGAGAACCCCTACCCCGG	745
QY	159	yAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysG	179
Db	746	CAACATACAGACACCATGTTGTGTGCCGGTGCAGAGAGGGGGCAAGGACTCCTGCCA	805
QY	179	nGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpG	199
Db	806	GGGTGACTCCGGGGGCTCTGTGTCTGTAAACAGTCTCTTCAAGGCATTATCTCCTGGG	865
QY	199	yGlnAspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyVa	219
Db	866	CCAGATCCGTTGCGATCACCCGAAAGCCCTGGTGTCTACACGAAAGTCTGCAATATGT	925
QY	219	laspTrpIleGlnGluThrMetLysAsnAsn	229
Db	926	GGACTGGATCCAGGACGATGAAGACAAT	956
RESULT 2			
BI818697			
LOCUS	603037514F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178746 5',		
DEFINITION	mRNA sequence.		
ACCESSION	BI818697		
VERSION	BI818697.1 GI:15930247		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 841)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Inyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11445 row: k column: 03 High quality sequence stop: 784.		

## FEATURES

## Location/Qualifiers

1. .841  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5178746"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC 115"  
 /note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORT6; Site\_1: NotI; site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,27e-106 Length: 841  
 Score: 1158.00 Matches: 222  
 Percent Similarity: 97.38% Conservative: 1  
 Best Local Similarity: 96.94% Mismatches: 1  
 Query Match: 92.05% Indels: 5  
 DB: 12 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BI818697 (1-841)

QY 6 GluCysLysProHisSerGln-ProTrpGlnAlaLeuPheGluLysThrArgLeuLe 25  
 Db 2 GAGTGCACGCTCATCCAGTCCCTGGCAGCAGCCCTGTTTCGAGAGAGCGGCTACT 61

QY 25 uCysGlyAlaThrLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysPr 45  
 Db 62 CTGTGGGGGCGAGCTCATCGCCCCAGATGGTCTCTGACAGAGCCCACTGCCTCAAGCC 121

QY 45 oArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnTh 65  
 Db 122 CGCTACATAGTTCACCTGGGCGAGCACACCTCCAGAGGAGGAGGCTGTGACGAC 181

QY 65 rArg-ThrAlaThrGluSerPheProHisProGlyPheAsnAspSerLeuProAsnLysA 85  
 Db 182 CTTGACAGCCCACTAGTCTTCCCGCCAGCCCGGCTTCAACACAGCTCCCCAACAAAG 241

QY 85 sPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer-IleThrTrpAla 104  
 Db 242 ACCACCGCAATGACATCATCTGCTGTAAGATGGCATCGCACTCTCTATCACCTGGGCT 301

QY 105 ValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSer 124  
 Db 302 GTGGACCCCTCACCTCTCTCACGCTGTGTCATGCTGGCAGCAGCTGCTCATTTTCC 361

QY 125 GlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsn 144  
 Db 362 GCTGGGCGAGCAGCTCCAGCCCCAGTACGCTGCTCTCACCTTCGATGGCCAC 421

QY 145 IleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThr 164  
 Db 422 ATCACCATATTGAGCACCAGAGGTGTGAGAACGCTTACCCCGGCAACATCACAGACAC 481

QY 165 MetValCysAlaSerValGlnGlu-GlyGlyLysAspSerCysGlnGlyAspSerGlyG 184  
 Db 482 ATGGTGTGTCAGGCTGCAGAGAGGGGGCAAGGACTCTCTGCCAGGTGACTCCGGGG 541

QY 184 yProLeuValCysAsnGlnSerLeuGln-GlyIleIleSerTrpGlyGlnAspProCysA 204  
 Db 542 CCTCTGCTGTAAACAGTCTCTTCAATGGCATTTATCTCTGGGGCGCAGGATCCGTGTG 601

QY 204 lalleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGln 224  
 Db 602 CGATCACCGAAAGCCTGGTGTCTACACGAAAGTCTGCAATATATGTGAGCTGGATCCAGG 661

QY 224 luThrMetLysAsnAsn 229  
 Db 662 AGACGATGAAGACAAT 678

## RESULT 3

## BI763040

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

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BI763040 678 bp mRNA linear EST 25-SEP-2001  
 603047838F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5187896 5',  
 mRNA sequence.

BI763040  
 BI763040.1 GI:15754618

EST.  
 EST.

Source  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens

REFERENCE  
 1 (Bases 1 to 678)

AUTHORS  
 NIH-MGC http://mgc.nci.nih.gov/.

TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
 Unpublished (1999)

COMMENT  
 Contact: Robert Strausberg, Ph.D.

Email: cgaops-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11469 row: h column: 09

High quality sequence stop: 647.

Location/Qualifiers

1. .678

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5187896"

/lab\_host="DH10B"

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/note="Organ: pooled colon, kidney, stomach; Vector:

PCMV-SPORT6; Site\_1: NotI; site\_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## Length:

## Matches:

## Conservative:

## Mismatches:

## Indels:

## Gaps:

## US-09-856-320A-2\_COPY\_54\_282 (1-229) x BI763040 (1-678)

## QY

## Db

## QY

## Db

## QY

## Db

## QY

## Db

## QY

## Db

## QY

## Db

130 GAGGAGGCTGTGAGCAGACCCGGACAGCAGCATGAGTCTCTCCGCCACCCCGGCTTCAAC 189  
QY AsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPro 98  
Db AACAGAGCTCCCAACAAACACACACCAATGACATCATCTGCTGTAAGATGGCATCGCA 249  
QY valSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGly 118  
Db GTCTCCATCACCTGGGCTGTGGACCCCTCACCTCTCTCACCTGTGTCTCTCTCTCTGC 309  
QY ThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHis 138  
Db ACCAGTGGCTCATTTCCGGCTGGGCGACAGCTCCAGCCCCCAGTTACGCTGCTCAC 369  
QY ThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpPro 158  
Db ACCTTGGATGCGCCCAACATCACCATCATTTGAGCAGACAGAGTGTGAGAACCCCTACCCC 429  
QY GlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCys 178  
Db GGCAACATCACAGACACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489  
QY GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 198  
Db CAGGTTGACTCCGGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 549  
QY GlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrp 218  
Db GGCCAGAGATCCGT 609  
QY ValAspTrpIleGlnGlnThrMetLysAsnAsn 229  
Db GTGCACTGGATCCAGGAGAGCATGAAGAACAT 642

RESULT 4  
BG720793 853 bp mRNA linear EST 08-MAY-2001  
LOCUS 602692015F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4824387 5',  
DEFINITION mRNA sequence.  
ACCESSION BG720793  
VERSION BG720793.1 GI:13999980  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 853)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M10735 Row: n Column: 04  
High quality sequence stop: 826.  
Location/Qualifiers  
1. 853  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4824387"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_97"  
/notes="Organ: testis; Vector: pBluescriptR (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI  
(gtcag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.2 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

ORIGIN  
Alignment Scores: 6.87e-105 Length: 853  
Pred. No.: 1141.00 Matches: 216  
Score: 1141.00 Conservative: 0  
Percent Similarity: 98.18% Mismatches: 3  
Best Local Similarity: 98.18% Indels: 2  
Query Match: 90.70% Gaps: 0  
DB: 12

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BG720793 (1-853)

QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
Db 196 ATCATCAAGGGGTTGAGTTCAGAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTTCGAG 255  
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
Db 256 AAGACGGGGTACTCTGTGGGGGAGCCTCATCGCCCGGAGATGGCTCTCTGACGAGGCC 315  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 316 CACTGCCCTCAAGCCCGCTCATAGTTACCTGGGGCAGCACCACTCCAGAGAGGAGGAG 375  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
Db 376 GGCTGTGAGCAGACCCGGACAGCAGCTGCTTCCCCCAGCCGGCTTCAACACAGC 435  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 436 CTCCTCCCAACAAAGACCCGCAATGATCATGCTGTGTGAAGATGGATGCCAGCTCTCC 495  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 496 ATCACTGGGGTGTGGAGCCCTCACCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 555  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 556 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTAGCCCTGCTCTACACCTTG 615  
QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160  
Db 616 CGATGGCGCAACATCACCATCATTTGAGCACCCAGAAAGTGTGAGAACGCTTACCCGGCAAC 675  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
Db 676 ATCAAGACACCATGGTGTGGCAGCGTGTGAGGAGGGGCAAGAGACTCTCTGCGAGTT- 734  
QY 181 AspSerGlyGlyProLeuVal-CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGly 200  
Db 735 GACTCCGGGGGCTCTGGTCTTGTAACTGCTTCTTCAAGGCAATTTATCTCCGGGTGCA 794  
QY 200 nAspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTrpVal 219  
Db 795 GGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTG 852

RESULT 5  
BM559782 1072 bp mRNA linear EST 20-FEB-2002  
LOCUS BM559782  
DEFINITION AGENCOURT\_6565460 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5744410  
5', mRNA sequence.  
ACCESSION BM559782  
VERSION BM559782.1 GI:18803655  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1072)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL2765 row: 1 column: 11  
High quality sequence stop: 684.

## FEATURES

## source

Location/Qualifiers

1..1072  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:574410"  
/tissue\_type="medulla"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 119"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: EcoRV (destroyed); RNA source normal medulla from  
anonymous male age 27. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.3 kb, insert size range  
0.9-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 013. Note:  
this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 7,9e-102 Length: 1072  
Score: 1112.50 Matches: 212  
Percent Similarity: 95.54% Conservative: 2  
Best Local Similarity: 94.64% Mismatches: 7  
Query Match: 88.43% Indels: 3  
DB: 12 Gaps: 1

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BM559782 (1-1072)

QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20  
DB 275 ATCATCAAGGGTTGAGTGCAGGCTCCTCCAGCCCTGCAGCGAGCCCTGTTCCAG 334  
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThAlaAla 40  
DB 335 AAGACGGGGCTACTCTGTGGGGCGAGCGCTCATCGCCCCAGATGCTCTGCACAGCAGCC 394  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60  
DB 395 CACTGCTTCAAGCCCGCTACATAGTTACCTGGGGCAGCAACCTCCAGAGGAGGAG 454  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 455 GCCTGTGAGCAGACCCGAGACCCACTGAGTCTTCCCCCCCGGGCTTCAACACAGC 514  
QY 81 LeuProAsnLysAspHisArgAsnAspLeuMetLeuValLysMetAlaSerProValSer 100  
DB 515 CTCCCCCAACAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCGCCAGTCTCC 574  
QY 101 lleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 575 ATCACTGNGCTGTGGACCCCTCACCCTCTCTCAGCTGTGTCTGCTGGACACAGC 634  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140

Db 635 TGCCCTATTTCGGCTGGGCGACGACGCTCCAGCCCCAGTTACGCTGCTCCACACCTTG 694  
QY 141 ArgCysAlaAsnIleThrIlelleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
Db 695 CGATCGCCCAACATCACCATTCATTGACACACAGAGTGTGAGAACGCTACCCCGGCAC 754  
QY 161 IleThrAspThrMetValCysAlaSerValGlnIleGlyLysAspSerCysGlnGly 180  
Db 755 ATCAGACACACCATGGTGTGTGCCAGCGTGCAGAGGGGGCAGGACTCCTGCNCAGGT 814  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly-Gl 200  
Db 815 GACTCCGGGGCCCTCTGGTCTGTATACCAAGTCTCTTCAAGGCATTATCTCTGGGGCCCA 874  
QY 200 nAspProCysAlaIleThrArgLysProGlyValTyrThr---LysValCysLysTyrVa 219  
Db 875 GGATCCGTGTGCGATCACCCGGAAGCCTGGTGTCTACCCGAAAGGTCTGCCAATATGT 934  
QY 219 1-AspTrp 221  
Db 935 GGGACTGG 942  
RESULT 6  
LOCUS AK009360 1295 bp mRNA linear HTC 20-SEP-2003  
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015I08 product:protease, serine, 20, full insert sequence.  
ACCESSION AK009360  
VERSION AK009360.1 GI:12844110  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
2  
REFERENCE  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
3  
REFERENCE  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kusunagi,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Hatada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
4  
REFERENCE  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
5  
REFERENCE  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)





QY 221 TTTTleGlnGluThrMetIysAsnAn 229  
 DB 945 TGGATCCAGGAGTTATGAGGAACAAT 971

RESULT 8  
 BM559617 1074 bp mRNA linear EST 20-FEB-2002  
 LOCUS AGENCOURT\_5565456 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5744314  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BM559617  
 VERSION BM559617.1 GI:18803348  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: LLAM12765 row: h column: 11  
 High quality sequence stop: 689.

FEATURES  
 Location/Qualifiers  
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 /clone\_lib="NIH\_MGC\_119"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: ScaRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1..17e-96 Length: 1074  
 Score: 1061.50 Matches: 212  
 Percent Similarity: 92.27% Conservative: 3  
 Best Local Similarity: 90.99% Mismatches: 12  
 Query Match: 84.38% Indels: 6  
 DB: 12 Gaps: 1

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BM559617 (1-1074)

QY 1 IleIleGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
 DB 274 ATCATCAAGGGTTTGAGTTCAGAGCTCATCTCCAGCCCTGGCAGCAGCCCTGTTCGAG 333

QY 21 LysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40  
 DB 334 AAGACGGGGTACTCTGTGGGGGCGAGCTCATCGCCCGCCAGATGGCTCTCGACAGCAGCC 393

QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
 DB 394 CACTGCTCAAGCCCGGCTACATAGTTTCCTGGGGGCGACCAACCTCCAGAGAGGAGG 453

QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80  
 DB 454 GGCTGTGAGCAGACCCGAGCAGCAGTCACTCTTCCCCACCCCGGCTTCAACACAGC 513

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 DB 514 CTCGCCAACAAAGACCAACCATGACATCATGTGTGTAAGATGGCATCGCAGTCTCC 573

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 DB 574 ATCACCTGGGCTGGCGACCCCTCACCTCTCTCAGCGTGTCTCATCTGTGCACACAGC 633

QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 DB 634 TGCCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGCCAGTTACGCTGCTCCACCTTG 693

QY 141 ArgCysAlaAsnIleThrIleGluHisGlnLysCysGluAsnAlaValProGlyAsn 160  
 DB 694 CGATCGCCCAACATCACCATTTGACACCAAGTGTGAGAACCGCTACCCCGGGCAC 753

QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly 180  
 DB 754 ATCACAGACCATCTGTGTGTGTCAGCGTGCAGGAGGGGGCAAGGACTCTCTGNCAGGGT 813

QY 181 AspSer-GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp-GlyG 200  
 DB 814 GACTCCGGGGGGCCCTCTGTGTGTGTTACCAAGTCTCTTCAAGGCAATTATCTCTCTGGGGGGC 873

QY 200 InAspProCys-AlaIleThrArgLys-ProGlyValThrLysValCysLysTrpVa 219  
 DB 874 AGNATCCGTGTGTCGATCACCCGAAAGCCCTGTGGCTACCCCAAAAGTCTTGCATAT 933

QY 219 1---AspTrpIle-GlnGluThrMetLys 227  
 DB 934 GTGGGACTGGATCCCGGAGACCATGGAG 962

RESULT 9  
 AK009659 1269 bp mRNA linear HTC 20-SEP-2003  
 LOCUS Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310037E23 product:protease, serine, 20, full insert sequence.  
 ACCESSION AK009659  
 VERSION AK009659.1 GI:12844589  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--394-format

sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
JOURNAL  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
JOURNAL  
REFERENCE  
AUTHORS

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AKO09659 (1-1269)

QY 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
Db 260 ATCATCAAGGGTTATGAGTTCAGCGCCCTCACACAGGCATGCGAGGTGGCCCTTTTCAG 319  
QY 21 LysThrArgLeuLeuCysGlyValAlaThrLeuIleAlaProAtgTTPLeuLeuThrAlaAla 40  
Db 320 AAGACACGGCTTCTCTGTGGGGCAACCCTCATCGCCCCCAANTGGCTCTTGACAGCAGCC 379  
QY 41 HisCysLeuLysProArgTyrlleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
Db 380 CACTCGGCCGAGCCCATTAAGTGTATCTCTTCAGAGACAATACTAGAGAGACAGAC 439  
QY 61 GlyCysGluGlnThrArgThralaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
Db 440 GGCTGTGAGCGAGG-CGGATGGCCACTGAG-CCITTCGCCACCCCGAGCTTTCACAAACAGC 498  
QY 81 LeuProAsnLysAspHisAargAsnAspileMetLeuValLysMetAlaSerProValSer 100  
Db 499 CTCGCCAACAAAGACCCCGGAATGACATAATGCTTGTGAAGATGTCTCTCCCGTCTTC 558  
QY 101 lleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 559 TTTACCCGAGCTGTGCAGCCCACTCACTCCCTGTCCCACACTGTGCTGTCAGGACACAGC 618  
QY 121 CysLeulleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 619 TGCTTCATTTCTGGATGGGACACACGTCAGCCGCCAGTTGGCGCTTCATTCCTTC 678  
QY 141 ArgCysAlaAsnIleThrIlelleGluHisGlnLysCysGluAsnAlaTyProGlyAsn 160  
Db 679 CGATGTGCCAATGTCTCCATCATCAACAACAGGAGTGTAGAAGGCTTACCGGGCAAC 738  
QY 161 lleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180  
Db 739 ATCAGACAGCCATCTGTGGCCAGTGTGGAAAGAGGCGAAGGACTCTCTGTGAGGT 798  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerleuGlnGlylleSerTrpGlyGln 200  
Db 799 GACTCTGAGGCGCCCTGGTCTGCAACGAGTCTTCAAGGCATCATCTCTCGGGGTGAG 858  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyThrLysValCysLysTyValAsp 220  
Db 859 GACCCATGTGCGCTCAGCAAGGCTGGTGTCTATACAAAGTCTGCAAAATCTTTTAAAC 918  
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
Db 919 TGGATCCAGAGGTATTGAGGAACAAT 945

RESULT 10  
AY410892  
LOCUS  
DEFINITION  
Homo sapiens KLK11 gene, VIRTUAL TRANSCRIPTr, partial sequence,  
genomic survey sequence.  
ACCESSION  
AY410892  
VERSION  
AY410892.1 GI:39766860  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Mammalia; Eutheria;  
Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE  
1 (bases 1 to 753)  
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F.F., Murphy,B.,  
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
JOURNAL  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
JOURNAL  
REFERENCE  
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1269)

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,  
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hiracka,T., Hori,F., Inotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,D.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5' GAGAGAGAGAGATCCAGAGCTTTTTTTTTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequence [5'  
GAGAGAGAGATTCGAGTTAAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved  
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.

Host: SOLR.  
Location/Qualifiers  
1. 1269  
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polyA\_signal  
1251..1256  
/note="putative"  
polyA\_site  
1269  
/note="putative"

misc\_feature  
polyA\_signal  
polyA\_site

ORIGIN

Alignment Scores:

Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 753)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
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 Score: 1008.00 Matches: 184  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.13% Indels: 0  
 DB: 29 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AY410892 (1-753)  
 QY 46 ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThr 65  
 DB 199 CGCTACATAGTTACCTGGGGGAGCAGCACTCCAGAGGAGGGCTGTGAGCAGAC 258  
 QY 66 ArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAsp 85  
 DB 259 CGGACAGCCACTGAGTCTCTCCCGCCACCCCGGGTTCACAAACAGCCTCCCAACAGAC 318  
 QY 86 HisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaVal 105  
 DB 319 CACCGCAATGACATCATCTGCTGGTGAAGATGGCATCGCCAGTCTCCATCATCCTGGGCTGTG 378  
 QY 106 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysteulleSerGly 125  
 DB 379 CGACCCCTCACCTCTCCTCACGCTGTGTCACTGCTGGCAGCAGCTGCTCTATTTCCGGC 438  
 QY 126 TrpGlySerThrSerProGlnLeuArgCysAlaAsnIle 145  
 DB 439 TGGGGGAGCAGCGTCCAGCCCCCAGTTACGGCTCCCTCAGCAGCTTGCAGTCCGCAACATC 498  
 QY 146 ThrIleIleGluHisGlnLysCysGluAsnAlaThrProGlyAsnIleThrAspThrMet 165  
 DB 499 ACCATCATTCAGCAGCAGAGAGTGTGAGACGCTACCCCGGCAACATCACAGACCATG 558  
 QY 166 ValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyGlyPro 185  
 DB 559 GTGTGTGCCAGCGTGCAGGAAGGGGCAAGGACTCTCTGCGAGGGTCACTCCCGGGCCCT 618  
 QY 186 LeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 205  
 DB 619 CTGGTCTGTAAACAGTCTCTTCAAGCAATATCTCTCTGGGGCCAGATCCGTTGGGATC 678  
 QY 206 ThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThr 225  
 DB 679 ACCCGAAGCGTGGTGTCTACACGAAAGTCTGAAATATGTGACTGTGATCCAGGAGAG 738  
 QY 226 MetLysAsnAsn 229  
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Db 739 ATGAAGAACAAAT 750  
 RESULT 11  
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 LOCUS  
 DEFINITION  
 Pan troglodytes KLX11 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 AY410893  
 ACCESSION  
 AY410893  
 VERSION  
 AY410893.1 GI:39766861  
 KEYWORDS  
 GSS.  
 SOURCE  
 Pan troglodytes (chimpanzee)  
 ORGANISM  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE  
 1 (bases 1 to 556)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
 1..556  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
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 <1..>556  
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 Score: 992.00 Matches: 180  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 97.83% Mismatches: 0  
 Query Match: 78.86% Indels: 0  
 DB: 29 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AY410893 (1-556)  
 QY 46 ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThr 65  
 DB 2 CGCTACATAGTTACCTGGGGGAGCAGCACTCCAGAGGAGGGCTGTGAGCAGAC 61  
 QY 66 ArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAsp 85  
 DB 62 CAGACAGCCACTGAGTCTCTCCCGCCACCCCGGGTTCACAGCAGCCTCCCAACAGAC 121  
 QY 86 HisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaVal 105  
 DB 122 CACCGCAATGACATCATCTGCTGGTGAAGATGGCATCGCCAGTCTCCATCATCCTGGGCTGTG 181  
 QY 106 ArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysteulleSerGly 125  
 DB 182 CGACCCCTCACCTCTCCTCACGCTGTGTCACTGCTGGCAGCAGCTGCTCTATTTCCGGC 241  
 QY 126 TrpGlySerThrSerProGlnLeuArgLysProHisThrLeuArgCysAlaAsnIle 145  
 DB 242 TGGGGGAGCAGCGTCCAGCCCCCAGTTACGGCTCCCTCACACCTTGGATCGGCAACATC 301  
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146 ThrileileGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMet 165  
302 ACCATCAITAGCACCAGAGGTGTGAGAACGGCTACCCCGGCAACATCACAGACACCATG 361  
166 ValCysAlaSerValGlnGluGlyCysGlnGlyValSerCysGlnGlyValSerGlyGlyPro 185  
362 GTGTGTGCAGCGTGGGGAAGGAGGACTCTCTCCAGGGGTGATCTCCGGGGGCCCT 421  
186 LeuValCysAsnGlnSerLeuGlnGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 205  
422 CTGGTCTGTAAAGAGTCTCTCAAGGCAITATCTCTCTGGGGCCAGGATCCATGTCCGATC 481  
206 ThrArgLysProGlyValThrLysValCysLysTyrValAspTrpIleGlnGluThr 225  
482 ACCCGAAACCTGGTGTCTACACGAAAGTCTGCAATATGTGGACTGGATCCAGAGACG 541  
226 MetLysAsnAsn 229  
542 ATGAGACAAAT 553

RESULT 12  
BG697071  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

602660281F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4803356 5',  
mRNA sequence.  
BG697071 GI:13962880  
EST.  
Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLA10699 row: a column: 21  
High quality sequence stop: 704.  
Location/Qualifiers  
1..708  
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Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

FEATURES  
source  
1..708  
Location/Qualifiers

ORIGIN  
Alignment Scores:  
Pred. No.: 1.77e-86 Length: 708  
Score: 958.00 Matches: 176  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 76.15% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BG697071 (1-708)

1 llaileylgylpheglucylcylslyprohiserglnprotrpglnalaleupheglu 20  
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178 ATCATCAAGGGTTCGATGTCAGAGCCTCATCCAGCCCTGGCAGGAGCCCTGTTTCGAG 237  
21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40  
238 AAGACGGCGGTACTCTGTGGGGCGACGCTCATGCCCCAGATGGCTCTCTAGACAGCACC 297  
41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
298 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACACCTCCAGAGAGGAGAG 357  
61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
358 GGCTGTGAGCAGACCCGCGACGACCTAGTCTCTTCCCCCACCCTCCGCTTCAACACAGC 417  
81 LeuProAsnLysAspHisArgAsnAspIleValLeuValLysMetAlaSerProValSer 100  
418 CTCCCCAACAAAGACCCGACCAATACATCATCTGCTGAAGATGGCATCGCCAGTCTCC 477  
101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
478 ATCACTGGGCTGTGGACCCCTCACCTCTCTCTCAGCTGTGTCACTGTGGCACCAGC 537  
121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
538 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCCCAGTTAGCCTGCTCCACCTTG 597  
141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
598 CGATGGCCCAACATCACCATTCATTGACACACAGAGTGTGAGACAGCTACCGCTCCCGGCAAC 657  
161 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAsp 176  
658 ATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGGAC 705

RESULT 13  
CF768612  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF768612 592 bp mRNA linear EST 17-OCT-2003  
CES002496 Bos taurus skin cDNA library Bos taurus cDNA clone  
CCL002496 5', mRNA sequence.  
CF768612  
CF768612.1 GI:37717831  
EST.  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 592)  
Wang, Y.H., McWilliam, S. and Lehnert, S.  
Transcription profiling of cattle skin  
Unpublished (2003)  
Contact: Dr Yonghong Wang  
Functional Genomics Lab  
CSIRO Livestock Industries  
Level 5, Queensland Biosciences Precinct, University of Queensland,  
306 Carmody Road St.Lucia QLD Australia  
Tel: 07 3214 2445  
Fax: 07 3214 2685  
Email: [Yonghong.Wang@csiro.au](mailto:Yonghong.Wang@csiro.au)  
Plate: 35 row: B column: 04.  
Location/Qualifiers  
1..592  
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/clone\_lib="Bos taurus skin cDNA library"  
/note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;

FEATURES  
source  
1..592  
Location/Qualifiers



Site 2: Xho I; Library made from pooled skin of adult female Hereford-Shorthorn."

# ORIGIN

Alignment Scores:  
 Pred. No.: 3,156-80 Length: 592  
 Score: 895.00 Matches: 156  
 Percent Similarity: 92.27% Conservative: 23  
 Best Local Similarity: 80.41% Mismatches: 15  
 Query Match: 71.14% Indels: 0  
 DB: 14 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x CF768612 (1-592)

Qy 36 LeuLeuThrAlaAlaHisCysLeuLeuProArgTyrIleValHisLeuGlyGlnHisAsn 55  
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 Qy 56 LeuGlnLysGluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisPro 75  
 Db 62 CTCGGGCGGAGGATGGCTGTGACAGCAGCGAAGTCCACCAAGTCTTCCCGCCACCA 121  
 Qy 76 GlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 95  
 Db 122 GACTTCAACAACAGCCCTCCCAACAAGACCCAGCAACGACATCATCTGGTGAAGATG 181  
 Qy 96 AlaserProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysVal 115  
 Db 182 GTGACCCCGCCCACTCCTGCGCTGTGCGACCCCTCACCCTGTCACCGCGCTGTGTG 241  
 Qy 116 ThrAlaGlyThrSerCysLeuLeuSerGlyTrpGlySerThrSerProGlnLeuArg 135  
 Db 242 CCGTCTGTGCGCACTGCTCTCACTTCGGCTGGGGCACCACCATGTCAGCCCCCAAGTGCAC 301  
 Qy 136 LeuProHisThrLeuArgCysAlaAsnIleThrIleLeuHisGlnLysCysGluAsn 155  
 Db 302 CTGCCCCATACCTTGGCATCGCCACAGTCACCATCATCAAGCACAGGAGTGTGAGGAC 361  
 Qy 156 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLys 175  
 Db 362 GCCTACCTGGCAACATCAGCAGACCATGTGTGTGCGCAGTGTCCGCAAGAGGCAAG 421  
 Qy 176 AspSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 195  
 Db 422 GACTCTTACCAGGCTGACTCTGGGGGCGCTCTGTCTGAACGGGTCTCTTCAAGGCATC 481  
 Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 215  
 Db 482 ATCTCTCTGGGGCGGAGGATCATGTGTGTCTCCAAAGAGCCTGGTGTATACAAAGGTC 541  
 Qy 216 CysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229  
 Db 542 TGCAAAATATGTGACTGGATCCAGAACACCATGAGACACAT 583

RESULT 14  
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 LOCUS AY410894  
 DEFINITION Mus musculus KLK11 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 mRNA sequence.  
 BG747134.1 GI:14057787  
 VERSION BG747134  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 639)  
 NIH-MGC <http://mgi.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 E-mail: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI710 row: k column: 14  
 High quality sequence stop: 638.  
 Location/Qualifiers  
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 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)";

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,256-76 Length: 639  
 Score: 852.00 Matches: 156  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.36% Mismatches: 0  
 Query Match: 67.73% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x BG747134 (1-639)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
 Db 168 ATCATCAGGGGTTGAGTGCAGAGCTCATCTCCAGGCTTGGCAGGAGCCCTGTTCAG 227  
 Qy 21 LysThrArgLeuLeuCysGlyAlaThrIleLeuAlaProArgTrpLeuLeuThrAlaAla 40  
 Db 228 AAGACGGGCTACTCTGTGGGGCAGCTCATGCCCCCGAGATGGCTCTTCAACACAGC 287  
 Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGluGlu 60  
 Db 288 CACTGCTCAAGCCCGCTCATAGTTCACTGGGGCAGCACAACCTCCAGAGAGGAGAG 347  
 Qy 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
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 Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 408 CTCCTCCCAACAAGACCCCGCAATGACATCATGTGTGAGATGGCATCGCAGTCTCC 467  
 Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 468 ATCACTGGGCTGTGGACCCCTTCCCTTCTCCTCAGCTGTGTCACTGTGGCAGCAGC 527  
 Qy 121 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 528 TGCCTCATTTCTGGGCTGGGGCAGCAGCTCAGGCCCGCCAGGTAGCTGCTGCCTCACAC 587  
 Qy 141 ArgCysAlaAsnIleThrIleLeuGluHisGlnLysCysGluAsnAlaTyr 157  
 Db 588 CGATGGCCCAACATCACCATCATTTGAGCAGCAGAGAGTGTGAGAGCGCTTAC 638

RESULT 15  
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 LOCUS AY410894  
 DEFINITION Mus musculus KLK11 gene, VIRTUAL TRANSCRIPT, partial sequence,



## genomic survey sequence.

ACCESSION AY410894  
 VERSION AY410894.1 GI:39766862  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 556)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering them based on alignment.

## FEATURES

## source

1..556 Location/Qualifiers

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 <1..>556  
 /gene="KLK11"  
 /locus\_tag="HCM4042"

## gene

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,33e-74 Length: 556  
 Score: 834.00 Matches: 147  
 Percent Similarity: 90.71% Conservative: 19  
 Best Local Similarity: 80.33% Mismatches: 17  
 Query Match: 66.30% Indels: 0  
 DB: 29 Gaps: 0

## US-09-856-320A-2\_COPY\_54\_282 (1-229) x AY410894 (1-556)

QY 47 TyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArg 66  
 Db 5 TACGTGATCTCTTGGAGAGACACATCTAGAGAGACAGCGGTGTGAGCAGAGCGG 64  
 QY 67 ThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHis 86  
 Db 65 ATGGCCACTGAGTCTCTCCCCACCCGACTTCAACACAGCGCTCCCAACAAGACCAC 124  
 QY 87 ArgAsnAspIleMetLeuValHisMetAlaSerProValSerIleThrTrpAlaValArg 106  
 Db 125 CGGAATGACATAATGTTGAGAGATGCTGCTCCCGTCTTTTACCAGCTGTGCAG 184  
 QY 107 ProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTirp 126  
 Db 185 CCACCTCACCTGTCCCCACACTGTGCTGCGTGCGAGCACCGCTGCTCATTTCTGGATGG 244  
 QY 127 GlySerThrSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThr 146  
 Db 245 GGCACCACTCCAGCCCGCAGTTGGCGCTGCCTCATTCCTCGCATGTGCCAATGTCTCC 304  
 QY 147 IleIleGluHisGlnLysCysGluAsnAlaTyProGlyAsnIleThrAspThrMetVal 166  
 Db 305 ATCATCGACACACAGAGATGTGAGAGGCTACCCGGGCAACATCACAGACCATGCTG 364  
 QY 167 CysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeu 186

Db 365 TGCGCCAGTGTTCGABAGAGGGCAAGGACTCTCTGTCTCAGGGTGACTCTCGAGGCCCCCTG 424  
 QY 187 ValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThr 206  
 Db 425 GTCTGTAACGGATCTCTTCAAGGCATCATCTCTGGGGTCAGGACCATGTGCGTCACC 484  
 QY 207 ArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMet 226  
 Db 485 AGAAGGCTGGTGTCTATACAAAAGTCTGCAATACTTTAACTGGATCCACGAGTTATG 544  
 QY 227 LysAsnAsn 229  
 Db 545 AGGAACAAT 553

Search completed: June 23, 2004, 03:51:40  
 Job time : 2965 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 18:52:07 ; Search time 45 Seconds  
(without alignments)  
1605.637 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258

Sequence: 1 IIKGPECKPHSQPWOALFE.....GVYTKVKYVDWIOETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organalle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235.5	98.2	275	4	Q8IXD7
2	1062	84.4	249	11	Q9QYN4
3	1062	84.4	276	11	Q9QYN3
4	883	54.3	260	4	Q8IW69
5	679	54.0	255	4	Q96RQ0
6	678	53.9	254	11	Q8CGR4
7	671.5	53.4	276	11	Q8CGR6
8	630	50.1	251	11	Q9DB08
9	623.5	49.6	293	11	Q9DI40
10	603	47.9	242	11	Q80V54
11	603	47.9	250	11	Q8CGR5
12	597.5	47.5	234	11	Q9CV76
13	590	46.9	246	11	Q9ZIR9
14	588	46.7	246	11	Q9QUK9
15	587.5	46.7	235	11	Q63274
16	587	46.7	246	11	Q9R0T7

17	583.5	46.4	239	11	Q63275	Q63275 rattus norv
18	581.5	46.2	261	11	Q9JW70	Q9JW70 mus musc
19	574.5	45.7	261	6	Q9N1Q1	Q9N1Q1 saguinus oe
20	574.5	45.7	261	6	Q29474	Q29474 canis fami
21	570.5	45.3	242	13	Q7TIR8	Q7TIR8 pangasius n
22	565.5	45.0	242	13	Q7SX90	Q7SX90 brachydanio
23	564.5	44.9	269	4	Q8IU55	Q8IU55 homo sapien
24	564	44.8	251	11	O54854	O54854 rattus norv
25	562.5	44.7	247	11	Q9CPN7	Q9CPN7 mus muscu
26	560.5	44.6	237	13	Q9I515	Q9I515 fugu rubrip
27	560.5	44.5	244	13	Q8QGW3	Q8QGW3 mus muscu
28	560	44.5	244	11	Q9I515	Q9I515 fugu rubrip
29	558.5	44.4	245	13	Q9I515	Q9I515 mus muscu
30	557	44.3	248	13	Q42160	Q42160 petromyzon
31	556.5	44.2	261	11	Q7SZT1	Q7SZT1 xenopus lae
32	556.5	44.2	263	11	Q8C232	Q8C232 mus muscu
33	556	44.2	263	11	Q9JW71	Q9JW71 mus muscu
34	556	44.2	240	13	Q98TH0	Q98TH0 engraulis j
35	556	44.2	243	13	Q7SZ06	Q7SZ06 xenopus lae
36	556	44.2	246	11	O88301	O88301 mus muscu
37	555.5	44.2	253	11	Q9IY82	Q9IY82 mus muscu
38	554.5	44.1	263	11	Q8AV11	Q8AV11 oncorhynch
39	554	44.0	262	4	Q86U61	Q86U61 mus muscu
40	552.5	43.9	244	13	O42159	O42159 petromyzon
41	552.5	43.9	254	6	Q9XSN6	Q9XSN6 sus scrofa
42	551.5	43.8	286	4	Q86TG8	Q86TG8 homo sapien
43	551	43.8	246	11	Q7TT42	Q7TT42 mus muscu
44	551	43.8	247	11	Q9CPN9	Q9CPN9 mus muscu
45	549.5	43.7	247	13	O42158	O42158 petromyzon

#### ALIGNMENTS

#### RESULT 1

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ID AC Q8IXD7 PRELIMINARY; PRT; 275 AA.  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Variant form hippostasin/KLK11.  
GN KLK11.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;  
RT "Molecular cloning and expression of a variant form of  
RT hippostasin/KLK11 in prostate.";  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB078780; BAC54105.1; -  
DR GO; GO:0004263; F:trypsin activity; IEA.  
DR GO; GO:0004295; F:chymotrypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SMC0020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
SQ SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;

Query Match 98.2%; Score 1235.5; DB 4; Length 275;  
Best Local Similarity 90.2%; Pred. No. 1,1e-122;  
Matches 229; Conservative 0; Mismatches 0; Indels 25; Gaps 1;

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 Db 22 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P W S L T S P T H V S P D L S 81  
 QY 46 ----- R Y I V H L G Q H N L O K E C E C T R A T E S F P H P G F N N S L P N K D H R N D I M L V K M 95  
 Db 82 S S N Y C U S H S R Y I V H L G Q H N L O K E C E C T R A T E S F P H P G F N N S L P N K D H R N D I M L V K M 141  
 QY 96 A S P V S I T W A R P L T L S R C V T A G T S C L I S G W G T S S P Q L R P H T L R C A N I T I I E H K C E N 155  
 Db 142 A S P V S I T W A R P L T L S R C V T A G T S C L I S G W G T S S P Q L R P H T L R C A N I T I I E H K C E N 201  
 QY 156 A P G N I T D T M V C A S V O E G K D S C Q D S G G P L V C N O S L O G I I S W G D P C A I T R K P G V Y T K V 215  
 Db 202 A P G N I T D T M V C A S V O E G K D S C Q D S G G P L V C N O S L O G I I S W G D P C A I T R K P G V Y T K V 261  
 QY 216 C K Y V D M I Q E T M K N 229  
 Db 262 C K Y V D M I Q E T M K N 275  
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 AC Q9QYN4;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Hippostasin.  
 GN PRS20.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Yamaguchi N., Mitsui S.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Mitsui S., Yamaguchi N.;  
 RL "cDNA cloning of a novel brain serine protease, Hippostasin.";  
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016226; BAA88825.1; -  
 DR HSP; P00763; IDPO.  
 DR MEROPS; S01.257; -  
 DR MGD; MG1:1929977; Prs20.  
 DR GO; GO:0005576; C:extracellular; IDA.  
 DR InterPro; IPR009003; Cys Ser trypsin.  
 DR InterPro; IPR001254; Peptidase S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPsin.  
 DR SMART; SMC0020; Tryp\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
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 Query Match 84.4%; Score 1062; DB 11; Length 249;  
 Best Local Similarity 81.2%; Pred. No. 2.5e-104;  
 Matches 186; Conservative 23; Mismatches 20; Indels 0; Gaps 0;  
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 Db 21 I I K G F E C K P H S Q P W Q A A L F E K T R L L C G A T L I A P R W L L T A A H C L K P R Y I V H L G Q H N L O K E E 80  
 QY 61 G C S Q T R T A T E S F P H P G F N N S L P N K D H R N D I M L V K M A S P V S I T W A R P L T L S R C V T A G T S 120  
 Db 81 G C S Q R M A T E S F P H P G F N N S L P N K D H R N D I M L V K M S S P V F F T R A V Q P L T L S P H C V A A G T S 140

QY 121 C L I S G W G T S S P Q L R P H T L R C A N I T I I E H K C E N A P G N I T D T M V C A S V O E G K D S C Q 180  
 Db 141 C L I S G W G T S S P Q L R P H S L R C A N W S I I E H K E K A P G N I T D T M L C A S V R E G K D S C Q 200  
 QY 181 D S G G P L V C N O S L O G I I S W G D P C A I T R K P G V Y T K V C K Y V D M I Q E T M K N 229  
 Db 201 D S G G P L V C N O S L O G I I S W G D P C A V T R K P G V Y T K V C K Y F N W I H E V M R N 249  
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 ID Q9QYN3  
 AC Q9QYN3;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Hippostasin prostate type (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert sequence).  
 GN PRS20.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Yamaguchi N., Mitsui S.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=20525460; PubMed=11072088;  
 RA Mitsui S., Okui A., Koninami K., Uemura H., Yamaguchi N.;  
 RT "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRS20).";  
 RL Biochim. Biophys. Acta 1494:206-210(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA Adachi J., Azawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shiragawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RT Nature 420:563-573(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Tongue;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;

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RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076961;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB016227; BAB36955.1; -.
DR EMBL; AK009360; BAB26241.2; -.
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DR HSSP; P00763; 1DPO.
DR MEROPS; S01.257; -.
DR MGD; MGI:192977; Prss20.
DR GO; GO:0005576; Cxetracellular; IDA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match 84.4%; Score 1062; DB 11; Length 276;
Best Local Similarity 81.2%; Pred. No. 2.8e-104;
Matches 186; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPWAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60
DB 48 IIKGECKPHSQPWAALFQKTRLLCGATLIAPRWLLTAHCKRPHYVILLGEHNLEKTD 107
QY 61 GCEQRTATSPFHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTS 120
DB 108 GCEQRMATESPFPFNNSLPNKDHNDIMLVKMASPVFFTRAQVPLTLSPHCVAAGTS 167
QY 121 CLISGWGSTSSPOLRLPHLCANITIIHCKENAYPGNITDTMVCASVOEGKDSQCG 180
DB 168 CLISGWGSTSSPOLRLPHLCANITIIHCKENAYPGNITDTMVCASVRKGDSCQ 227
QY 181 DSGGLVLCNQSLOGIISWGQDPICAITRPGVYTKVCKYVDWIQETMKN 229
DB 228 DSGGLVLCNQSLOGIISWGQDPICAVTRKPGVYTKVCKYFNMHEVRNN 276

RESULT 4
Q8IW69 ID Q8IW69 PRELIMINARY; PRT; 260 AA.
AC Q8IW69;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

"High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20530913; PubMed=11076961;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB016227; BAB36955.1; -.
DR EMBL; AK009360; BAB26241.2; -.
DR EMBL; AK009720; BAB26461.2; -.
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DR MEROPS; S01.257; -.
DR MGD; MGI:192977; Prss20.
DR GO; GO:0005576; Cxetracellular; IDA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match 54.3%; Score 683; DB 4; Length 260;
Best Local Similarity 51.8%; Pred. No. 4.2e-64;
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGECKPHSQPWAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGHNLOKEE 60
DB 33 VLGHECHQSPQWAALFQGGQLCGVLGVGNWVLTAAHCKKPKYTVRLGDHSLQNKD 92
QY 61 GCEQRTATSPFHPGFNNSLPNKDHNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTS 120
DB 93 GPEQETPVQSIHPHPCVNSS-DVEDENHDLMLQLRDQASLGSKVKPISLADHCTQPGQK 151
QY 121 CLISGWGSTSSPOLRLPHLCANITIIHCKENAYPGNITDTMVCASVOEGKDSQCG 180
DB 152 CTVSGMGVTVSPRENFPDLTNCVAEVKIFPKKCEDAYPGQITDMVVCAGSSKGA-DTCQ 210
QY 181 DSGGLVLCNQSLOGIISWGQDPICAITRPGVYTKVCKYVDWIQET 224
DB 211 DSGGLVLCGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKK 254

RESULT 5
Q96RQO ID Q96RQO PRELIMINARY; PRT; 255 AA.
AC Q96RQO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prostinoogen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT degenerate PCR.";
RL Biochemistry 40:1679-1687(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF303046; AAK62813.1; -.
DR HSSP; P00761; 1AN1.
DR MEROPS; S01.081; -.
DR GO; GO:0004263; F.chymotrypsin activity; IEA.
DR GO; GO:0008233; F.peptidase activity; IEA.

```



QY 123 ISGWGSSPQLRPHLTHLRCANITIEHOKCENAYPGNITDTMVCSASVOEGGKDCSGDS 182  
DB 160 VSGMTTSPQNYKPTLQCANIELRDEBECQVYFGKITANMLCAGTKEGGKDCSGDS 219  
QY 183 GGPLVCSQLOGIISWGQDPFCATRKPGVYTKVKYVDWIQETMKN 228  
DB 220 GGPLICNGKLYGISWGDFPGQPNRPVYTVSKYLWIREIRN 265  
RESULT 8  
Q9DBQ8  
ID Q9DBQ8 PRELIMINARY; PRT; 251 AA.  
AC Q9DBQ8;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE 1200016C12RIK protein.  
GN 1200016C12RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Lung;  
RC MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AK04807; BAB23579.1; -;  
DR HSSP; P00763; IDPO.  
DR MEROPS; S01.307; -;  
DR MGD; MGI:1921082; 1200016C12RIK.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
KW Hydroxylase; Protease; Serine protease.  
SQ SEQUENCE 251 AA; 28153 MW; F4D667F8C80C4A23 CRC64;

Query Match 50.1%; Score 630; DB 11; Length 251;  
Best Local Similarity 52.7%; Pred No. 1.7e-50;  
Matches 118; Conservative 36; Mismatches 78; Indels 0; Gaps 0;  
QY 6 ECKPHSQPQAALFKRLTLCATLIAPRWLLTAHCRKPYLWVLRGEHHLWRWEGPEQL 87  
DB 66 RTATESFPHPGNNLSLPKNDHNDIMLVKMASPVSTWAVRLTLSSRCVTAGTSCLLISG 125  
DB 88 LLYVTDFFPHGPNLSANDHNDIMLIRLPKRVLTJPAVQPLNLTESPPVGTQCLIFG 147  
QY 126 WGSTSSPQLRLPHTLRCAITIEHOKCENAYPGNITDTMVCSASVOEGGKDCSGDS 185  
DB 148 WGSVSSSKLOYPMTLQCANISILDNKFRCWAYPGHIFKILCAGLWEGGSGCQDGGP 207  
RESULT 9  
Q9D140  
ID Q9D140 PRELIMINARY; PRT; 293 AA.  
AC Q9D140;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE 110030019RIK protein.  
GN 110030019RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Embryo;  
RC MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AK003996; BAB23113.1; -;  
DR HSSP; P00763; IDPO.  
DR MEROPS; S01.017; -;  
DR MGD; MGI:1915918; 110030019RIK.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydroxylase; Protease; Serine protease.  
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D9226FE911 CRC64;









Qy	114	CVTAGTSLISGWSTSSPQLRPLPHTLRCA	NIIEHOKCENAYPGNITDTMVCASVOEG	173
Db	119	BPXVGTCLVSGWSTKPLISELPDDLOQ	CVNIDLLSNEKTEAYRWKVTDLMLCAGLEG	178
Qy	174	GKDSGQDSGGPLVNCNSLOGIISWGQDP	CAITRXPVYTKVCKYVDWIOETMKN	229
Db	179	GKDACNGDSGGPLICDGLQGLTSWGS	VPCGEPHNPFIYTKIIFTSWIKVMKEN	234

Search completed: June 22, 2004, 18:56:20  
Job time : 47 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 18:48:16 ; Search time 60 Seconds  
(without alignments)  
1078.390 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Sequence: 1 IIRGFECRPHSQPWQALFE.....GVYTKYCKYDVTIGETMKON 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	3 AAB21325	Aab21325 Human TLS
2	1258	100.0	250	3 AAY99390	Aay99390 Human PRO
3	1258	100.0	250	4 AAB66139	Aab66139 Protein o
4	1258	100.0	250	4 AAU12424	AAU12424 Human PRO
5	1258	100.0	250	4 ABB50479	ABb50479 Human sec
6	1258	100.0	250	5 AAU83684	AAu83684 Human PRO
7	1258	100.0	250	5 ABB84920	ABb84920 Human PRO
8	1258	100.0	250	5 ABB95526	ABb95526 Human ang
9	1258	100.0	250	5 ABO17868	ABo17868 Novel hum
10	1258	100.0	250	6 ABB80831	ABb80831 Human PRO
11	1258	100.0	250	6 ABO33797	ABo33797 Novel hum
12	1258	100.0	250	6 ABB81122	ABb81122 Human PRO
13	1258	100.0	250	6 ABB56739	ABb56739 Lung can
14	1258	100.0	250	6 ABB66822	ABb66822 Human PRO
15	1258	100.0	250	6 ABB59903	ABb59903 Novel sec
16	1258	100.0	250	6 ABO25093	ABo25093 Human sec
17	1258	100.0	250	6 ABB82140	ABb82140 Novel hum
18	1258	100.0	250	6 ABB67098	ABb67098 Human sec
19	1258	100.0	250	6 ABB46025	ABb46025 Novel hum
20	1258	100.0	250	6 ABB76456	ABb76456 Human PRO
21	1258	100.0	250	6 ABB72320	ABb72320 Human PRO
22	1258	100.0	250	6 ABB19106	ABb19106 Human PRO
23	1258	100.0	250	6 ABB61729	ABb61729 Homo sapi
24	1258	100.0	250	6 ABB19514	ABb19514 Novel hum
25	1258	100.0	250	6 ABB19514	ABb19514 Novel hum

## ALIGNMENTS

26	1258	100.0	250	6 ABB28055	ABb28055 Human PRO
27	1258	100.0	250	6 ABB86534	ABb86534 Novel hum
28	1258	100.0	250	6 ABB16098	ABb16098 Human PRO
29	1258	100.0	250	6 ABB47884	ABb47884 Human PRO
30	1258	100.0	250	6 ABB044736	ABb044736 Novel hum
31	1258	100.0	250	6 ABB033632	ABb033632 Novel hum
32	1258	100.0	250	6 ABB67679	ABb67679 Human PRO
33	1258	100.0	250	6 ABB30686	ABb30686 Human PRO
34	1258	100.0	250	6 ABB85982	ABb85982 Novel hum
35	1258	100.0	250	6 ABB97194	ABb97194 Human PRO
36	1258	100.0	250	6 ABB79498	ABb79498 Human PRO
37	1258	100.0	250	6 ABB87637	ABb87637 Novel hum
38	1258	100.0	250	6 ABB16839	ABb16839 Human PRO
39	1258	100.0	250	6 ABB91931	ABb91931 Novel hum
40	1258	100.0	250	6 ABB14994	ABb14994 Human PRO
41	1258	100.0	250	6 ABB18955	ABb18955 Novel hum
42	1258	100.0	250	6 ABB94470	ABb94470 Human PRO
43	1258	100.0	250	6 ABB20066	ABb20066 Novel hum
44	1258	100.0	250	6 ABB13378	ABb13378 Human PRO
45	1258	100.0	250	6 ABB043401	ABb043401 Novel hum

RESULT 1  
AAB21325  
ID AAB21325 standard; protein; 250 AA.

AC AAB21325;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human TLSP.

KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; TLSP;  
KW trypsin-like serine protease; kallikrein-like protein; serine protease;  
KW cytosolic; cancer; prostate cancer.

XX OS Homo sapiens.  
XX  
PN WO2000053776-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-CA000258.

PR 11-MAR-1999; 99US-0124260P.  
PR 01-APR-1999; 99US-0127386P.  
PR 21-JUL-1999; 99US-0144919P.

XX (MOUN ) MOUNT SINAI HOSPITAL.  
XX  
XX Yousef GW, Diamandis EP;  
XX WPI; 2000-587440/55.

XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L  
XX protein mediated disorders, especially cancer.  
XX  
XX Example 5; Fig 27; 184pp; English.

XX The present sequence is human trypsin-like serine protease (TLSP), a  
XX member of the serine protease family. Kallikreins and kallikrein-like  
XX proteins are a subgroup of the serine protease enzyme family. They  
XX catalyze the selective cleavage of specific polypeptide precursors to  
XX release peptides with potent biological activity. Nucleic acids encoding  
XX kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-  
XX L6 have been isolated. The proteins are useful in the treatment,  
XX monitoring and diagnosis of cancers, especially prostate cancer. They  
XX can also be used to identify a substance that can associate with or  
XX mediate the biological activity of the proteins. Antibodies can be used  
XX to treat conditions mediated by the kallikrein-like proteins



PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
 PR 17-NOV-1998; 98US-0108788P.  
 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108867P.  
 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.

PA (GETH ) GENENTECH INC.

XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;

DR WPI; 2000-237871/20.

DR N-PSDB; AAA37072.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 12; Fig 102; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 3; Length 250;

Best Local Similarity 100.0%; Pred. No. 2.8e-112;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPQALFEKTRLLCGATLIPRMLTAHCLKPRIVLHGHNLQKEE 60  
 Db 22 IIKGECKPHSQPQALFEKTRLLCGATLIPRMLTAHCLKPRIVLHGHNLQKEE 81  
 QY 61 GCEQRTATATESPPHGFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 120  
 Db 82 GCEQRTATATESPPHGFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 141  
 QY 121 CLISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGGKDSQCG 180  
 Db 142 CLISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGGKDSQCG 201  
 QY 181 DSGGPLVNCNOSLOGIISWGDPACATIRKPGVYTKVCKYVDWIQETMKNN 229  
 Db 202 DSGGPLVNCNOSLOGIISWGDPACATIRKPGVYTKVCKYVDWIQETMKNN 250

RESULT 3  
 AAB6139  
 ID AAB6139 standard; protein; 250 AA.

XX AAB6139;  
 AC AAB6139;

XX 02-APR-2001 (first entry)  
 DT Protein of the invention #51.  
 XX  
 DE Secreted; transmembrane; gene therapy.  
 XX  
 KW Unidentified.  
 XX  
 OS WO200078961-A1.  
 XX  
 PN 28-DEC-2000.  
 XX  
 PD 18-FEB-2000; 2000WO-US004342.  
 PF  
 XX 23-JUN-1999; 99US-0144037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Pan W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK;  
 PI Williams PM, Wood WT;

DR WPI; 2001-071395/08.

XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.

XX Claim 1; Fig 102; 787pp; English.

XX The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 4; Length 250;

Best Local Similarity 100.0%; Pred. No. 2.8e-112;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPQALFEKTRLLCGATLIPRMLTAHCLKPRIVLHGHNLQKEE 60  
 Db 22 IIKGECKPHSQPQALFEKTRLLCGATLIPRMLTAHCLKPRIVLHGHNLQKEE 81  
 QY 61 GCEQRTATATESPPHGFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 120  
 Db 82 GCEQRTATATESPPHGFNNSLPNKDHNDIMLVKASPVSTIWAVERPLTSSRCVTAGTS 141  
 QY 121 CLISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGGKDSQCG 180  
 Db 142 CLISGSGTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVQEGGKDSQCG 201  
 QY 181 DSGGPLVNCNOSLOGIISWGDPACATIRKPGVYTKVCKYVDWIQETMKNN 229  
 Db 202 DSGGPLVNCNOSLOGIISWGDPACATIRKPGVYTKVCKYVDWIQETMKNN 250

RESULT 4

AAU12424  
 ID AAU12424 standard; protein: 250 AA.  
 XX  
 AC AAU12424;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO1279 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIa; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US032678.  
 XX  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 06-JAN-2000; 2000WO-US000377.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023528.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 XX  
 PA (GENTECH) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W,  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21496.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 other PRO polypeptides, link bioactive molecules to cells expressing PRO

PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
 PT breast, prostate, cervical.  
 XX  
 PS Claim 12; Fig 506; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful to detect other PRO  
 CC polypeptides, to link bioactive molecules to cells expressing PRO  
 CC polypeptides, to modulate biological activities of cells expressing PRO  
 CC polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample. Some  
 CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIa. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy  
 CC  
 SQ Sequence 250 AA:  
 Query Match 100.0%; Score 1258; DB 4; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112; Indels 0; Gaps 0;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIKGFECRPHSQPQWALFEKTRLLCGATLLAPRMLTAAHCLPRYIVHGHNLQKEE 60  
 DB 22 IIKGFECRPHSQPQWALFEKTRLLCGATLLAPRMLTAAHCLPRYIVHGHNLQKEE 81  
 QY 61 GCEQRTITSEPPHGFENSLPNKQDRDILVYKASPVSTTAVRPLTSSRCVYTGTS 120  
 DB 82 GCEQRTITSEPPHGFENSLPNKQDRDILVYKASPVSTTAVRPLTSSRCVYTGTS 141  
 QY 121 CLISGSGTSSPOLRLPPTLRCAITITIEHCKENAYPGNTTDMVCAVQEGSKDSQCG 180  
 DB 142 CLISGSGTSSPOLRLPPTLRCAITITIEHCKENAYPGNTTDMVCAVQEGSKDSQCG 201  
 QY 181 DSGGPLVGNOSLGGTISWGDPICAITRRKPGYTKVCKYVDMTQTKMN 229  
 DB 202 DSGGPLVGNOSLGGTISWGDPICAITRRKPGYTKVCKYVDMTQTKMN 250  
 RESULT 5  
 ABB50479  
 ID ABB50479 standard; protein: 250 AA.  
 XX  
 AC ABB50479;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
 XX  
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;  
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 KW cytoskeletal; cardiant; vascular; anti-angiogenic; ophthalmological;  
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;  
 KW antiparkinsonian; antitubercular; gene therapy; vaccine; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;  
 KW Gaucher's disease; cardiovascular disease; Schmitzer syndrome; chemotaxis;  
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;  
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease.  
 XX  
 OS Homo sapiens.



XX MO200162891-A2.  
 XX 30-AUG-2001.  
 PD 21-FEB-2001; 2001WO-US005614.  
 XX 24-FEB-2000; 2000US-0184836P.  
 PR 29-MAR-2000; 2000US-0193170P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI Ni J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;  
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;  
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CJ, Ferris AM, Fan P;  
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z;  
 PI Greene JM;  
 XX WPI; 2001-625724/72.  
 DR N-PSDB; ABA83372.  
 XX  
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease  
 PT and diabetic retinopathy.  
 XX  
 PS Claim 11; Page 1181-1182; 1533pp; English.  
 XX  
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted  
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Example of these activities include: immunomodulatory; antisclerotic;  
 CC dermatological; immunosuppressive; anti-inflammatory; antitumor;  
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;  
 CC neuroprotective; neurotrophic; anticonvulsant; antialzheimer's; vascular;  
 CC antiparkinsonian; antidiabetic; and vulnerary. (I) and (II) can be used  
 CC in gene therapy and vaccine production. (I) and (II) can be used in the  
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 CC Gaucher's disease), cardiovascular diseases (e.g. Schmitt's syndrome,  
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiocentric  
 CC disorders (e.g. corneal graft neovascularization and diabetic  
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 4; Length 250;  
 Best Local Similarity 100.0%; Pired. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IIKGFECKPSPQWALFEKTRLLCGATLIAPRMILTAHCKPRIVYIHLGHNOKXE 60  
 22 IIKGFECKPSPQWALFEKTRLLCGATLIAPRMILTAHCKPRIVYIHLGHNOKXE 81  
 61 GCEOTRTATSPFPFGNNSLPNKDHNDIMLVKASPVSTIAVRPLTSSRCVTAAGTS 120  
 82 GCEOTRTATSPFPFGNNSLPNKDHNDIMLVKASPVSTIAVRPLTSSRCVTAAGTS 141  
 121 CLISGWSSTSPQRLPHTLRCAITITIEHOKENAPGNTITPWCASVQEGKSCOG 180  
 142 CLISGWSSTSPQRLPHTLRCAITITIEHOKENAPGNTITPWCASVQEGKSCOG 201  
 181 DSGGPLVQNSLOGIISWGQDPCATIRKPKSVYTRKVCYVWIOETWKN 229  
 202 DSGGPLVQNSLOGIISWGQDPCATIRKPKSVYTRKVCYVWIOETWKN 250

RESULT 6  
 AAU83684

ID AAU83684 standard; protein; 250 AA.  
 AC AAU83684;  
 DT 08-MAY-2002 (first entry)  
 DE Human PRO protein, Seq ID No 186.  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha.  
 OS Homo sapiens.  
 PN MO200208288-A2.  
 XX 31-JAN-2002.  
 PD 29-JUN-2001; 2001WO-US021066.  
 PF 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220585P.  
 PR 25-JUL-2000; 2000US-0220605P.  
 PR 25-JUL-2000; 2000US-0220607P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220638P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 25-JUL-2000; 2000US-0220666P.  
 PR 26-JUL-2000; 2000US-0220893P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 01-AUG-2000; 2000US-0222425P.  
 PR 22-AUG-2000; 2000US-0227133P.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023528.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 28-NOV-2000; 2000US-0253646P.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001WO-US017092.  
 XX  
 PA (GENENTECH INC).  
 XX  
 PI Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 DR WPI; 2002-172001/22.  
 DR N-PSDB; ABA833628.  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumors such  
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
 PT or liver tumor.  
 XX  
 PS Claim 11; Fig 186; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
 CC liver tumor. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
 CC protein sequences of the invention

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 5; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 60  
 DB 22 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 81

QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141

QY 121 CLISGWSGTSPPQLRPHTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDSGCG 180  
 DB 142 CLISGWSGTSPPQLRPHTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDSGCG 201

QY 181 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 229  
 DB 202 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDMIOETMKN 250

# RESULT 7

ABG61816 standard; protein; 250 AA.

XX ABG61816;

XX 15-AUG-2002 (first entry)

XX Prostate cancer-associated protein #17.

XX Prostate cancer; prostate tumour tissue; human; mammal; cyrostatic.

XX Mammalia.

XX WO200230268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

XX 08-DEC-2000; 2000US-00733288.

XX 08-DEC-2000; 2000US-00733742.

XX 24-JAN-2001; 2001US-0263957P.

XX 16-MAR-2001; 2001US-0276791P.

XX 16-MAR-2001; 2001US-0276888P.

XX 06-APR-2001; 2001US-0281922P.

XX 24-APR-2001; 2001US-0286214P.

XX 30-APR-2001; 2001US-00847046.

XX 04-MAY-2001; 2001US-0288589P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevez F,

XX WPI; 2002-471335/50.

XX N-PSDB; AK92131.

XX Detecting a prostate cancer-associated transcript in a cell in a patient,  
 XX useful for diagnosing prostate cancer (PC) or screening modulators of PC,  
 XX by determining if prostate cancer-associated genes are expressed in a  
 XX prostate tissue.

XX Claim 27; Page 314; 436P; English.

XX

CC The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated PC genes) that selectively  
 CC hybridise to a sequence that is at least 80% identical to them. The  
 CC prostate cancer-associated polynucleotide sequences are differentially  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 5; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 60  
 DB 22 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 81

QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141

QY 121 CLISGWSGTSPPQLRPHTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDSGCG 180  
 DB 142 CLISGWSGTSPPQLRPHTLRCAANTITIEHCKENAYPGNITDTMVCASVQEGKDSGCG 201

QY 181 IIKGFECCKPHSQPQALFEKTRLLCGATLIAAPRMILTAHCLKPRYIVHLGQHNLOKEE 229  
 DB 202 DSGGFLVNCOSLQGIISWGDPICAITRKPGVYTKVCKYVDMIOETMKN 250

# RESULT 8

ABB84920 standard; protein; 250 AA.

XX ABB84920;

XX 16-MAY-2002 (first entry)

XX Human PRO1279 protein sequence SEQ ID NO:208.

XX Human; angiogenesis; cardiant; cyrostatic; antiangiogenic; hypotensive;

XX vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;

XX angiotensin disorder; cardiac hypertrophy; atherosclerosis; hypertension;

XX age-related macular degeneration; arterial restenosis; angina;

XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;

XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

XX wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

17-AUG-2000; 2000US-00643657.  
 ER 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00766498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX  
 XX (GETH ) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88175.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 208; 565bp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC anging, myocardial infarctions, thrombophilicis, lymphangitis, tumor  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention

XX Sequence 250 AA:

Query Match 100.0%; Score 1258; DB 5; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFEEKPHSQPQALFETRLCGATLIAPWMLTAHCKPRIVLHGGHNOKEE 60  
 Db 22 IIKGFEEKPHSQPQALFETRLCGATLIAPWMLTAHCKPRIVLHGGHNOKEE 81  
 QY 61 GCEQTRTATESFPHPGNNNSIPKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 120  
 Db 82 GCEQTRTATESFPHPGNNNSIPKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 141

QY 121 CLISGWGSTSSPOLRLPHTLRCAITIIIEHOKENAYPNDITDWCASVQSGKDCOG 180  
 Db 142 CLISGWGSTSSPOLRLPHTLRCAITIIIEHOKENAYPNDITDWCASVQSGKDCOG 201  
 QY 181 DSGGPLVNCOSLOGIISKQDPCATIRKPGVYTKVCKYVDIOETWKN 229  
 Db 202 DSGGPLVNCOSLOGIISKQDPCATIRKPGVYTKVCKYVDIOETWKN 250

#### RESULT 9

ABB85526  
 ID ABB95526 standard; protein; 250 AA.

XX ABB95526;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 XX antiarteriosclerotic.

OS Homo sapiens.

PN WO200208284-A2.

XX 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00665350.

PR 18-SEP-2000; 2000US-00664610.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 10-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00766498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 30-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 01-JUN-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX 20-JUN-2001; 2001WO-US019692.

XX (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FER/) FERRARA N.

PA (GER/) GERBER H.

PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLMAN K U.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX Baker KP, Ferrara N, Gardner H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W.  
XX WPI, 2002-171999/22.  
XX N-PSDB; AB195664.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.  
XX Claim 11, Fig 208; 567pp; English.  
XX The present invention provides the protein and coding sequences of human CC PRO proteins. These are useful for treating or diagnosing a CC cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, CC angina, myocardial infarctions, thrombophlebitis, lymphatic, tumour CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention  
XX SQ Sequence 250 AA;  
Query Match 100.0%; Score 1258; DB 5; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2.8e-112; Mismatches 0; Gaps 0;  
Matches 229; Conservative 0; Indels 0;  
QY 1 IIKGECKPHSQPMALFEKTRLLCGATLIPAPMLTAAHCKPRIVHIGQHNLOKEE 60  
DB 22 IIKGECKPHSQPMALFEKTRLLCGATLIPAPMLTAAHCKPRIVHIGQHNLOKEE 81  
QY 61 GCEQRTTTSFPPHGFNNSLPNKDRNDIMLVMAASPVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTTTSFPPHGFNNSLPNKDRNDIMLVMAASPVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCKENAVPGNITDTMVCASVQEGKDCSQG 180  
DB 142 CLISGSGSTSSPOLRLPHTLRCAITIIHOKCKENAVPGNITDTMVCASVQEGKDCSQG 201  
QY 181 DSGGLVNOGLQGIISWGDPICATIRPGYITVKCYKVMIOGTMMKN 229  
DB 202 DSGGLVNOGLQGIISWGDPICATIRPGYITVKCYKVMIOGTMMKN 250  
RESULT 10  
ID ABO17868 standard; protein, 250 AA.  
XX ABO17868;  
XX 26-AUG-2003 (first entry)  
XX Novel human secreted and transmembrane protein PRO1279.  
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;  
XX antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
XX antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
XX TNF-alpha release; cell proliferation; cell differentiation;  
XX gene expression modulator; proteoglycan release; cytokine release;

KW tumour; inflammatory disease; organ failure; atherosclerosis;  
KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
KW bioreactor; tissue typing.  
XX Homo sapiens.  
XX US2003032156-A1.  
XX 13-FEB-2003.  
XX 06-MAY-2002; 2002US-00140474.  
XX 31-MAR-1997; 97WO-US005230.  
XX 12-JUN-1998; 98WO-US012456.  
XX 14-JUL-1998; 98WO-US014552.  
XX 28-AUG-1998; 98WO-US017888.  
XX 10-SEP-1998; 98WO-US018824.  
XX 14-SEP-1998; 98WO-US019093.  
XX 14-SEP-1998; 98WO-US019177.  
XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
XX 29-OCT-1998; 98WO-US022931.  
XX 20-NOV-1998; 98WO-US024855.  
XX 01-DEC-1998; 98WO-US025108.  
XX 05-JAN-1999; 99WO-US000106.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99WO-US005190.  
XX 20-APR-1999; 99WO-US008615.  
XX 14-MAY-1999; 99WO-US010733.  
XX 02-JUN-1999; 99WO-US012252.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
XX 13-SEP-1999; 99WO-US020944.  
XX 15-SEP-1999; 99WO-US021090.  
XX 05-OCT-1999; 99WO-US021547.  
XX 29-NOV-1999; 99WO-US023089.  
XX 02-DEC-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
XX 30-NOV-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028564.  
XX 02-DEC-1999; 99WO-US028565.  
XX 16-DEC-1999; 99WO-US030099.  
XX 20-DEC-1999; 99WO-US030911.  
XX 20-DEC-1999; 99WO-US030999.  
XX 22-DEC-1999; 99WO-US030720.  
XX 30-DEC-1999; 99WO-US031243.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000277.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 24-FEB-2000; 2000WO-US004914.  
XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005746.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 10-MAR-2000; 2000WO-US006319.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 20-MAR-2000; 2000WO-US007377.  
XX 21-MAR-2000; 2000WO-US007332.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WMO-US014042.  
 PR 30-MAY-2000; 2000WMO-US014941.  
 PR 02-JUN-2000; 2000WMO-US015264.  
 PR 28-JUL-2000; 2000WMO-US020710.  
 PR 11-AUG-2000; 2000WMO-US022031.  
 PR 23-AUG-2000; 2000WMO-US023522.  
 PR 24-AUG-2000; 2000WMO-US023328.  
 PR 08-NOV-2000; 2000WMO-US030952.  
 PR 10-NOV-2000; 2000WMO-US030873.  
 PR 01-DEC-2000; 2000WMO-US032678.  
 PR 20-DEC-2000; 2000WMO-US034956.  
 PR 20-DEC-2000; 2000WMO-US034956.  
 PR 28-FEB-2001; 2001WMO-US0796498.  
 PR 28-FEB-2001; 2001WMO-US006520.  
 PR 01-MAR-2001; 2001WMO-US006666.  
 PR 09-MAR-2001; 2001WMO-US006666.  
 PR 14-MAR-2001; 2001US-00802706.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001US-00871092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WMO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WMO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WMO-US020116.  
 PR 29-JUN-2001; 2001WMO-US021066.  
 PR 09-JUL-2001; 2001WMO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 PR XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2003-341980/32.  
 DR N-PSDB: ACD24105.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, for treating  
 PT inflammation, organ failure, atherosclerosis, cardiac injury,  
 PT infertility, birth defects, premature aging, acquired immunodeficiency  
 PT syndrome (AIDS), or cancer.  
 PS  
 XX  
 PS Claim 12; Fig 506; 660pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid (I) comprising, or which  
 CC has 80 % sequence identity to, or the full-length coding sequence of, one  
 CC of 275 nucleotide sequences, and which encodes a corresponding  
 CC polypeptide selected from 275 amino acid sequences, where all sequences  
 CC are given in the specification. The polypeptide encoded by (I) is used to  
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
 CC release of tumor necrosis factor (TNF)-alpha from human blood, modulate  
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
 CC the proliferation or differentiation of cells or gene expression,  
 CC stimulate the release of proteoglycans, stimulate the release of cytokine  
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
 CC to factor VIIa, or detect the presence of tumor in a mammal. The nucleic  
 CC acid and polypeptide encoded by it, are useful for treating inflammatory  
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
 CC birth defects, premature aging, acquired immunodeficiency syndrome

CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
 CC hybridisation probes, in chromosome and gene mapping, and in generating  
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
 CC This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide  
 XX  
 SQ Sequence 250 AA;  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIRGFECRPHSQWQALFEKTRLLCGATLIPRMLITAAHLKPRYIVHLCQNIQKEE 60  
 DB 22 IIRGFECRPHSQWQALFEKTRLLCGATLIPRMLITAAHLKPRYIVHLCQNIQKEE 81  
 QY 61 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTS 120  
 DB 62 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKASPVSTWAVRPLTLSSRCVTAGTS 141  
 QY 121 CLISGWSTSSPOLRLPHTLRCAITIIIEHCKENAVPENITDTWVCASVQSGKDSGCG 180  
 DB 142 CLISGWSTSSPOLRLPHTLRCAITIIIEHCKENAVPENITDTWVCASVQSGKDSGCG 201  
 QY 181 DSGGPLVCNQSLOGIISWGDPCATTRKRGVYTKYCKYVDWIOETMKN 229  
 DB 202 DSGGPLVCNQSLOGIISWGDPCATTRKRGVYTKYCKYVDWIOETMKN 250  
 RESULT 11  
 ABUS0831  
 ID ABUS0831 standard; protein; 250 AA.  
 XX  
 AC ABUS0831;  
 XX  
 DT 23-JUN-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #93.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036635-A1.  
 PD 20-FEB-2003.  
 PF 28-AUG-2002; 2002US-00230163.  
 PR 25-JUL-2000; 2000US-0220638P.  
 PR 01-JUN-2001; 2001WMO-US017800.  
 PR 29-JUN-2001; 2001WMO-US021066.  
 PR 09-APR-2002; 2002US-00119480.  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2003-342045/32.  
 DR N-PSDB: ACA66933.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for the manufacture of a medicament for diagnosing or treating  
 PT tumor.  
 PS  
 PS Claim 11; Fig 186; 314pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO

CC polypeptides and polynucleotides are useful for preparing a medicament  
 CC useful in the diagnosis and treatment of tumors. Anti-PRO antibodies are  
 CC useful in diagnostic assays for PRO, by detecting its expression in  
 CC specific cells, tissues or serum, and for affinity purification of PRO  
 CC from recombinant cell culture or natural sources. AB080739-AB080860  
 CC represent the human PRO polypeptides of the invention. Note: The sequence  
 CC data for this patent was obtained in electronic format directly from the  
 CC USPTO web site at [seqdata.uspto.gov/psipdidentry.html](http://seqdata.uspto.gov/psipdidentry.html)  
 XX

SO Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 6; Length 250;

Best Local Similarity 100.0%; Pred. No. 2.8e-112; Indels 0; Gaps 0;  
 Matches 229; Conservative 0; Mismatches 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLIAPRMILTAAHCKPRYIVHGGHNLQKEE 60  
 DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLIAPRMILTAAHCKPRYIVHGGHNLQKEE 81  
 QY 61 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGWSTSSPOLRPLPHTLRCAVNTIIIEHCKENAYPGNITDTMVCASVQEGKDCSCG 180  
 DB 142 CLISGWSTSSPOLRPLPHTLRCAVNTIIIEHCKENAYPGNITDTMVCASVQEGKDCSCG 201  
 QY 181 DSGGPLVNCNOSLGGIISWGDDPCATITKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNOSLGGIISWGDDPCATITKPGVYTKVCKYVDWIOETMKN 250

RESULT 12  
 ABO33797  
 ID ABO33797 standard; protein; 250 AA.

XX ABO33797;

DT 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1279.

XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;  
 XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;  
 XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;  
 XX colon tumour; breast tumour; prostate tumour; rectal tumour;  
 XX liver tumour; bone disorder; cartilage disorder; sports injury;  
 XX arthritis; wound.

XX Homo sapiens.

XX US2003045687-A1.

XX 06-MAR-2003.

PF 12-AUG-2002; 2002US-00218631.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX (GETH ) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-512315/48.

XX N-PSDB; ACD68685.

PT New genes, and its encoded secreted and transmembrane polypeptides,  
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or  
 PT pericyte proliferation, especially for treating lung tumors, arthritis or

PT wounds in a mammal.  
 XX  
 PS Claim 11; Fig 166; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a  
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of  
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are  
 CC fully defined in the specification; or (b) any of 122 nucleotide  
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the  
 CC specification; or the full length coding sequence of any these 122  
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful  
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are  
 CC particularly useful for detecting tumours (e.g. lung tumour, colon  
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)  
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,  
 CC for stimulating the proliferation or differentiation of chondrocyte  
 CC cells, for stimulating proliferation of pericyte cells, or for modulating  
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or  
 CC polypeptide is also useful for treating tumours or various bone and/or  
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The  
 CC PRO polypeptides are useful in drug screening, particularly as targets  
 CC for therapeutic intervention in these diseases. The PRO polypeptides are  
 CC also useful as molecular weight markers, or for chromosome  
 CC identification. The PRO genes are useful as hybridisation probes, or for  
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may  
 CC also be used in gene therapy, particularly for replacing a defective  
 CC gene. This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide  
 XX  
 SO Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112; Indels 0; Gaps 0;  
 Matches 229; Conservative 0; Mismatches 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLIAPRMILTAAHCKPRYIVHGGHNLQKEE 60  
 DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLIAPRMILTAAHCKPRYIVHGGHNLQKEE 81  
 QY 61 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIITWAVRPLTSSRCVTAGTS 141  
 QY 121 CLISGWSTSSPOLRPLPHTLRCAVNTIIIEHCKENAYPGNITDTMVCASVQEGKDCSCG 180  
 DB 142 CLISGWSTSSPOLRPLPHTLRCAVNTIIIEHCKENAYPGNITDTMVCASVQEGKDCSCG 201  
 QY 181 DSGGPLVNCNOSLGGIISWGDDPCATITKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNOSLGGIISWGDDPCATITKPGVYTKVCKYVDWIOETMKN 250

RESULT 13

AB081122  
 ID AB081122 standard; protein; 250 AA.

XX AB081122;

DT 23-JUN-2003 (first entry)

DE Human PRO polypeptide #253.

XX Human; PRO polypeptide; secreted and transmembrane protein;  
 XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;  
 XX bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
 XX sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
 XX hearing loss; coagulation disorder; stroke; heart attack; candida;  
 XX anti-diabetic; anorectic; vulnerable; antiarthritic; osteopathic;  
 XX anti-neumatic; auditory; cerebroprotective; angiogenic.  
 XX Homo sapiens.

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Page 11

PN	052003004311.A1.	
XX	02-JAN-2003.	
PD		
XX		
PF	19-DEC-2001; 2001US-00028072.	
XX		
PR	18-JUN-1997; 97US-0049911P.	
PR	26-AUG-1997; 97US-0056974B.	
PR	17-SEP-1997; 97US-0059113B.	
PR	17-SEP-1997; 97US-0059115P.	
PR	17-SEP-1997; 97US-0059112P.	
PR	17-SEP-1997; 97US-0059184P.	
PR	18-SEP-1997; 97US-0059263P.	
PR	19-SEP-1997; 97US-0059352P.	
PR	19-SEP-1997; 97US-0059585B.	
PR	14-SEP-1997; 97US-0059636P.	
PR	17-OCT-1997; 97US-0062250P.	
PR	17-OCT-1997; 97US-0062285P.	
PR	17-OCT-1997; 97US-0063755P.	
PR	24-OCT-1997; 97US-0062814P.	
PR	24-OCT-1997; 97US-0062816P.	
PR	24-OCT-1997; 97US-0063045P.	
PR	24-OCT-1997; 97US-0063082P.	
PR	24-OCT-1997; 97US-0063127P.	
PR	27-OCT-1997; 97US-0063327P.	
PR	27-OCT-1997; 97US-0063329P.	
PR	28-OCT-1997; 97US-0063350P.	
PR	28-OCT-1997; 97US-0063561P.	
PR	29-OCT-1997; 97US-0063704P.	
PR	29-OCT-1997; 97US-0065846P.	
PR	29-OCT-1997; 97US-0066373P.	
PR	29-OCT-1997; 97US-0066438P.	
PR	30-OCT-1997; 97US-0064378P.	
PR	30-NOV-1997; 97US-0064388P.	
PR	07-NOV-1997; 97US-0064609P.	
PR	12-NOV-1997; 97US-0065186P.	
PR	11-NOV-1997; 97US-0065464P.	
PR	21-NOV-1997; 97US-0066364P.	
PR	24-NOV-1997; 97US-0066453P.	
PR	24-NOV-1997; 97US-0066511P.	
PR	11-DEC-1997; 97US-0066470P.	
PR	11-DEC-1997; 97US-0066512P.	
PR	11-DEC-1997; 97US-0069278P.	
PR	16-DEC-1997; 97US-0069348P.	
PR	23-DEC-1998; 97US-0076564P.	
PR	23-JAN-1998; 97US-0077220P.	
PR	04-FEB-1998; 97US-0073612P.	
PR	09-FEB-1998; 97US-0074086P.	
PR	09-FEB-1998; 97US-0074092P.	
PR	12-MAR-1998; 97US-0077719P.	
PR	20-MAR-1998; 97US-0078910P.	
PR	25-MAR-1998; 97US-0079294P.	
PR	27-MAR-1998; 97US-0079663P.	
PR	27-MAR-1998; 97US-0079728P.	
PR	12-JUN-1998; 97US-0080165P.	
PR	28-AUG-1998; 97US-0080145P.	
PR	24-NOV-1998; 97US-0051788B.	
PR	10-SEP-1998; 97US-00518824.	
PR	14-SEP-1998; 97US-00519093.	
PR	14-SEP-1998; 97US-0051917P.	
PR	14-SEP-1998; 97US-00519330.	
PR	17-SEP-1998; 97US-00519437.	
PR	07-OCT-1998; 97US-00521141.	
PR	23-OCT-1998; 97US-00522992.	
PR	23-OCT-1998; 97US-00522992.	
PR	20-NOV-1998; 97US-00524855.	
PR	01-DEC-1998; 97US-0052510P.	
PR	03-JAN-1999; 97US-0052010P.	
PR	08-MAR-1999; 97US-0050502B.	
PR	10-MAR-1999; 97US-0050519P.	

20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021099.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 16-DEC-1999; 99WO-US028565.  
PR 20-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 30-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.

(GENTECH ) GENENTECH INC.  
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX MPI, 2003-352836/33.  
DR N-PsDB; ACN67246.

New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or heart attack.

Claim 12; Fig 50c; 643pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g., rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinemia, hearing loss, and coagulation disorders (e.g., stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABH80870-ABU8114 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/patseqIdentify.html

Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 6; Length 250;  
Best local Similarity 100.0%; Pred. NO. 2.8e-112;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 IIKFECKPHSQPQALAFKTRLLCGATLIPAWMLIAAHCLKRPYIVHLGQNTLKEE 60  
DB 22 IIKFECKPHSQPQALAFKTRLLCGATLIPAWMLIAAHCCLKRPYIVHSGQNTLOEE 81

QY 61 GCEOTRTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIITWAVRLTSSRCVTAGTS 120  
 DB 82 GCEOTRTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIITWAVRLTSSRCVTAGTS 141  
 QY 121 CLISGSGTSSPOLRLPHTLRCAITIIHOKCENAPGNTIDTMCASVOEGKDSGCG 180  
 DB 142 CLISGSGTSSPOLRLPHTLRCAITIIHOKCENAPGNTIDTMCASVOEGKDSGCG 201  
 QY 181 DSGGPLVNCNQLGGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 250  
 RESULT 14  
 ABUS6739  
 ID ABUS6739 standard; protein; 250 AA.  
 AC ABUS6739;  
 XX 02-APR-2003 (first entry)  
 DE Lung cancer-associated polypeptide #332.  
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;  
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX Unidentified.  
 OS W020286443-A2.  
 PN W020286443-A2.  
 PD 31-OCT-2002.  
 XX 18-APR-2002; 2002MO-US012476.  
 PF 18-APR-2001; 2001US-0284770P.  
 XX 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-034370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA Aziz N, Murray R;  
 PI WPI: 2003-093161/08.  
 DR N-PSDB; ABX76468.  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX Claim 27; Page 443-444; 453pp; English.  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell  
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
 CC for diagnostic purposes and as targets for screening for therapeutic  
 CC compounds that modulate lung cancer, such as antibodies. Sequences  
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
 CC invention  
 CC  
 XX Sequence 250 AA;  
 SQ  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2,8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIRGFECKPHSQPQALFEKTRLLGATLIAPRWLTAAHCKPRYIVHAGHNLOKEE 60  
 DB 22 IIRGFECKPHSQPQALFEKTRLLGATLIAPRWLTAAHCKPRYIVHAGHNLOKEE 81  
 QY 61 GCEOTRTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIITWAVRLTSSRCVTAGTS 120  
 DB 82 GCEOTRTATESFPHPGFNNSLPNKDRNDIMLVKASPVSIITWAVRLTSSRCVTAGTS 141  
 QY 121 CLISGSGTSSPOLRLPHTLRCAITIIHOKCENAPGNTIDTMCASVOEGKDSGCG 180  
 DB 142 CLISGSGTSSPOLRLPHTLRCAITIIHOKCENAPGNTIDTMCASVOEGKDSGCG 201  
 QY 181 DSGGPLVNCNQLGGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229  
 DB 202 DSGGPLVNCNQLGGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 250  
 RESULT 15  
 ABUS6822  
 ID ABUS6822 standard; protein; 250 AA.  
 AC ABUS6822;  
 XX 23-MAY-2003 (first entry)  
 DE Human PRO polypeptide #253.  
 XX Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.  
 XX Homo sapiens.  
 OS US2003036180-A1.  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 XX 09-MAY-2002; 2002US-00143114.  
 PF 31-MAR-1997; 97WO-US005230.  
 XX 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017868.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 14-SEP-1998; 98WO-US019437.  
 PR 15-SEP-1998; 98WO-US019430.  
 PR 17-SEP-1998; 98WO-US021141.  
 PR 07-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 29-OCT-1998; 98WO-US024855.  
 PR 20-NOV-1998; 98WO-US025108.  
 PR 01-DEC-1998; 98WO-US000106.  
 PR 05-JAN-1999; 99WO-US005028.  
 PR 08-MAR-1999; 99WO-US005190.  
 PR 10-MAR-1999; 99WO-US008615.  
 PR 20-APR-1999; 99WO-US010733.  
 PR 14-MAY-1999; 99WO-US012252.  
 PR 02-JUN-1999; 99WO-US020111.  
 PR 01-SEP-1999; 99WO-US020111.



PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028213.  
 PR 30-NOV-1999; 99WO-US028493.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030939.  
 PR 22-DEC-1999; 99WO-US030720.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000377.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US000365.  
 PR 18-FEB-2000; 2000WO-US000431.  
 PR 18-FEB-2000; 2000WO-US000432.  
 PR 22-FEB-2000; 2000WO-US000414.  
 PR 24-FEB-2000; 2000WO-US000414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005001.  
 PR 02-MAR-2000; 2000WO-US005746.  
 PR 10-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006319.  
 PR 20-MAR-2000; 2000WO-US006884.  
 PR 21-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US007532.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023528.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US047259.  
 PR 20-DEC-2000; 2000WO-US043456.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872835.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882632.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.

PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927996.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX  
 PA (GENTH) GENENTECH INC.  
 XX  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,  
 XX  
 DR WPI; 2003-332040/31.  
 DR N-PDB; ACN03855.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
 PT typing, and in chromosome identification.  
 XX  
 XX  
 PS Claim 12; Fig 506; 660pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for for-  
 CC identifying agonists or antagonists. The PRO polypeptides are useful for  
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
 CC human blood, for stimulating the proliferation or differentiation of  
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
 CC in chromosome and gene mapping, in the generation of antisense RNA and  
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic  
 CC animals or knockout animals, for the genetic analysis of individuals with  
 CC genetic disorders, and in gene therapy. AB06570-AB06684 represent the  
 CC human PRO polypeptides of the invention. Note: The sequence data for this  
 CC patent was obtained in electronic format directly from the USPTO web site  
 CC at seqdata.uspto.gov/psipdsidEntry.html  
 XX  
 SQ Sequence 250 AA;  
 Query Match 100.0%; Score 1258; DB 6; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-112;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIKGFECCKPHSQPQALFEKTRILCGATILAPRWLITRAHCLKRKYIVHIGQNLQEE 60  
 DB 22 IIKGFECCKPHSQPQALFEKTRILCGATILAPRWLITRAHCLKRKYIVHIGQNLQEE 81  
 QY 61 GCEQRTATIESPFPHPGPNNSLPNKDHRNDIMLVKASPVSLTWAVRPYTLSSRCVTAGTS 120  
 DB 82 GCEQRTATIESPFPHPGPNNSLPNKDHRNDIMLVKASPVSLTWAVRPYTLSSRCVTAGTS 141  
 QY 121 CLISMGSTSSPQLPPLHTLCANTTIEHOKCEYAGNITDPMVCAVSVEGGDSOG 180  
 DB 142 CLISMGSTSSPQLPPLHTLCANTTIEHOKCEYAGNITDPMVCAVSVEGGDSOG 201  
 QY 181 DSGGPLVNCNOSLGGIISWGODPCATIRKPGVYTKVCKYVDVIOETMKN 229  
 DB 202 DSGGPLVNCNOSLGGIISWGODPCATIRKPGVYTKVCKYVDVIOETMKN 250

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 Job time : 63 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 18:52:42 ; Search time 20 Seconds

(without alignments)  
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Title: US-09-856-320A-2\_COPY\_54\_282

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Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1: \*\*  
2: p1r2: \*\*  
3: p1r3: \*\*  
4: p1r4: \*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684	54.4	260	2	156559
2	605.5	48.1	265	1	KORP
3	600.5	47.7	261	2	A31136
4	595.5	47.3	261	1	NGMSG
5	594	47.2	248	2	S55066
6	591.5	47.0	263	2	S15686
7	591	47.0	246	1	TRRT2
8	588	46.7	238	2	S31779
9	587	46.7	246	1	TRRT1
10	585.5	46.5	261	2	A34079
11	581.5	46.2	259	2	B31136
12	578	45.9	232	1	KOPG
13	577.5	45.9	261	2	A29586
14	577.5	45.9	261	2	A29745
15	577	45.9	231	1	TRPGMR
16	574.5	45.7	261	2	S45303
17	571	45.4	246	2	B25528
18	568	45.1	249	1	TRDG
19	567.5	45.1	259	1	KQRTN
20	565.5	44.9	261	2	A25606
21	564.5	44.9	244	2	A44284
22	564.5	44.9	261	1	KOMSI
23	564	44.8	229	1	TRBORR
24	562	44.7	262	1	KOHU
25	560	44.5	248	2	S55067
26	556.5	44.2	257	2	S33772
27	556.5	44.2	261	2	S01971
28	556	44.2	243	2	A35871
29	556	44.2	247	2	S13813

30	553	44.0	247	2	A27547	trypsin (EC 3.4.21
31	552.5	43.9	231	2	S31778	trypsin (EC 3.4.21
32	552.5	43.9	247	2	S05494	trypsin (EC 3.4.21
33	552	43.9	256	1	NGMSA	7S nerve growth fa
34	551.5	43.8	239	2	A27207	tissue kallikrein
35	551.5	43.8	261	1	A32297	semogelase (EC 3
36	550	43.7	246	1	TRDGC	trypsin (EC 3.4.21
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38	548.5	43.6	261	1	S35711	semogelase (EC 3
39	548.5	43.6	261	2	A41020	tissue kallikrein
40	548.5	43.6	253	2	A53968	serine proteinase
41	544.5	43.3	242	2	S31775	trypsin (EC 3.4.21
42	544.5	43.3	242	2	S49489	trypsin (EC 3.4.21
43	544.5	43.3	242	2	S31776	trypsin (EC 3.4.21
44	543.5	43.2	261	2	JB0236	tissue kallikrein
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## ALIGNMENTS

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RESULT 1
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neutropsin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: 156559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, T.; Niehri
U: Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease ger
A:Reference number: 156559; PMID:9534817; PMID:7623137
A:Accession: 156559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D30785; NID:g1648847; PIDN:BA06451.1; PID:g1020091
A:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

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Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

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QY 61 GGEQRTATSPFPHGPNNSLPNKDHRNDIVLVKASPVSTWAVRPLTSSRCVTAGTS 120
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Db 93 QPEQRTQAQSTQHCCTVNSNP-EDHSIDIMLRQNSANIGDKYKPVQLANLCRKVGQK 151
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QY 121 CUISGSGTSPQRLPHTLRCANITIEHKCENAVPGNITDITVNCASVQEGKDSQGG 180
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Db 152 CIIISGVTSPQENFPNTLNCABVYKSNKCEKAYGKITEGVNCAAG-SSNGADTQGG 210
   :::::::::::::::::::::
QY 181 DSGGFLVNCQSLQGIISWGQDPCATRRKPGVYTVKCKYVDMIQETMKN 228
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Db 211 DSGGFLVCDGMLQGITWSGSDPCGKPEKPGVYTKICRYTTWIKTMDN 258
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RESULT 2
KORP
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 16-Jun-2000
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of
A:Reference number: A00944; PMID:83117659; PMID:9661406
A:Accession: A00944
A:Molecule type: mRNA
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D5 149 EPRKVGSTCLAGWMSITFPDGLSELDLDCVNNIDLLSNKECAVEAHKEEVTIDMLCAGEMDG 208  
 QY 174 GKSDCGGSGGGLPVLCNOSLOGIISMGDPCATIRPGVYTVCKVMDIOETMKN 229  
 D5 209 GKDTCKGSGGPLLCNGVLGITSMGFNPGCEPKKPGIYLYLIRFTPIKEVMEN 264  
 RESULT 3  
 A1136  
 tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat  
 NAlternate names: glandular prokallikrein 7, submandibular; proteinase A  
 CSpecies: Rattus norvegicus (Norway rat)  
 CDate: 31-Mar-1990 #sequence revision 31-Mar-1990 #text\_change 22-Jun-1999  
 CAccession: A11136; S10698; S10699; D41429; B41429; S09315  
 RChen, Y.P.; Chao, J.; Chao, L.  
 Biochemistry 27, 7189-7196, 1988  
 ATitle: Molecular cloning and characterization of two rat renal kallikrein genes.  
 AReference number: A11136; MUID:89088074; PMID:2849988  
 AAccession: A11136  
 A:Molecule type: DNA  
 A:Residues: 1-261 <CHE>  
 A:Cross-references: GB:M19647; GB:J02837; MID:G204999; PIDB:AAA41461.1; PID:G205000  
 R:Elmouhamed, A.; Gutman, N.; Brillard, M.; Gauchier, F.  
 FEBS Lett. 265, 137-140, 1990  
 ATitle: Substrate specificity of two kallikrein family gene products isolated from the  
 A:Reference number: S10698; MUID:90306305; PMID:2194829  
 AAccession: S10698  
 A:Molecule type: Protein  
 A:Residues: 25-36 <ELM>  
 AAccession: S10699  
 A:Molecule type: Protein  
 A:Residues: 1-261 <EL2>  
 R:Kato, H.; Nakamishi, E.; Enjyoji, K.; Hayaishi, I.; Oh-Ishi, S.; Iwanaga, S.  
 J. Biochem. 102, 1389-1404, 1987  
 ATitle: Characterization of serine proteinases isolated from rat submaxillary gland: w  
 A:Reference number: A41429; MUID:88198057; PMID:3482210  
 AAccession: D41429  
 A:Molecule type: Protein  
 A:Residues: 1-213 <KAT>  
 AAccession: B41429  
 A:Molecule type: Protein  
 A:Residues: 25-34 'D', 36-45 'S', 47-67 'X', 69-75 <KX2>  
 R:Brady, J.M.; MacDonald, R.J.  
 Arch. Biochem. Biophys. 278, 342-349, 1990  
 ATitle: The expression of two kallikrein gene family members in the rat kidney.  
 A:Reference number: S09315; MUID:90225801; PMID:2183721  
 AAccession: S09315  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 43-45 'S', 47-114 'A', 116-261 <BR>  
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 CKeywords: hydrolase; serine proteinase  
 F.1.18/Domain: signal sequence #status predicted <SIG>  
 F.19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>  
 F.25-253/Domain: trypsin homology <TRY>  
 F.65,120,213/Active site: His, Asp, Ser #status predicted  
 Query Match 47.7%; Score 600.5; DB 2; Length 261;  
 Best Local Similarity 46.2%; Pred. No. 7.4e-46;  
 Matches 109; Conservative 39; Mismatches 81; Indels 7; Gaps 1;  
 QY 1 IIKGFEEKPSOPQALFEKTRLLGCATLIAPMLTAAACHLPRYIVHLGCHLCEE 60  
 D5 25 VLGKYEKESQRPQVALYSEFTKYLCCGVLLDEPWTIAHCSNNTQVMGRNNLDE 84  
 QY 61 GCEQGTATSPHPHGNNSL-----PKDRNDIMLVKMASPVSTIAVRPLTSSR 113  
 D5 85 PFAQHRIVLVSQFPRDPYKPLMRNHTRRPGDGHENDMLLHLSQPADITDGAVKIDLPTE 144  
 QY 114 CVYAGNSCLISGWSGSSPOLRLPHTLRCANITIEHCKENAYRGNITDMVCASVQEG 173  
 D5 145 EPRVGSGTCLAGWMSITFPDGLSELDLDCVNNIDLLSNKECAVEAHKEEVTIDMLCAGBIEG 204

QY 174 GKDSGCGDGGPVLVNCOSLOGIISWGDPICATIRKPGYVTKYKXVDMIOETMKN 229  
 Db 205 GKDTCTGDSGGPILCDGVLOGITSWGSPVPCAKTNMFAITKILKFTSWIKVEWKEN 260

## RESULT 4

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Dec-1981 #sequence\_revision 17-May-1985 #ext\_change 18-Jun-1999

C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705

R:Evans, B.A.; Richards, R.I.

EMBO J 4, 133-138, 1985

A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contiguous

A:Reference number: A91005; MUID:85257431; PMID:3848399

A:Accession: A91005

A:Molecule type: DNA

A:Residues: 1-261 <EVA>

R:Ulrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.

DNA 3, 387-392, 1984

A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth factor

A:Reference number: A90949; MUID:85076183; PMID:6548955

A:Accession: A90949

A:Molecule type: mRNA

A:Residues: 1-261 <ULL>

R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.

Nucleic Acids Res 12, 2791-2805, 1984

A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to

A:Reference number: A93510; MUID:84169573; PMID:6200835

A:Accession: A93510

A:Molecule type: mRNA

A:Residues: 127-202 'E', 204-261 <HOW>

A:Cross-references: GB:X00472; NID:954260; PIDN:CAA25154.1; PID:954261

A:Experimental source: Inbred strain DBA/2J

R:Thomas, K.A.; Baglan, N.C.; Bradshaw, K.A.

J. Biol. Chem. 256, 9156-9166, 1981

A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S ne

A:Reference number: A92341; MUID:81264363; PMID:7263706

A:Accession: A92341

A:Molecule type: protein

A:Residues: 25-107, 112-261 <THO>

A:Experimental source: Outbred strain Swiss Webster

C:Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed

C:Comment: The active form of the gamma chain occurs naturally as combinations of either

C:Genetics:

A:Map position: 7

A:Intons: 16/1; 165/2; 165/1; 210/3

C:Superfamily: trypsin; trypsin homology

C:Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gla

F:1-18/Domain: signal sequence #status predicted <SIG>

F:25-253/Domain: trypsin homology <TRY>

F:25-107/Domain: segment B1 <GB1>

F:25-107, 112-261/Product: nerve growth factor gamma chain (active form) #status experime

F:112-261/Domain: segment A <GA>

F:112-164/Domain: segment C <GCC>

F:165-261/Domain: segment B2 <GB2>

F:31-173, 50-66, 152-219, 184-198, 209-234/Disulfide bonds: #status predicted

F:65, 120, 213/Active site: His, Asp, Ser #status predicted

F:102/Binding site: carbohydrate (asn) (covalent) #status experimental

QY 114 CVTAGTSLISWGSGTSBPQLRLPHLLRCATITIIHQKCNAYPGNITDVMCAVOEG 173  
 Db 145 EPLKASTCLASGKSGITRTKQFPDDLCVNLKLLPNEDCAKAIHKVTDMLCAGENDG 204

QY 174 GKDSGCGDGGPVLVNCOSLOGIISWGDPICATIRKPGYVTKYKXVDMIOETMKN 229  
 Db 205 GKDTCTGDSGGPILCDGVLOGITSWGHTPCGEPDMPGVYTKXKFTSWIKDTAKN 260

RESULT 5

5S5066  
 trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken

N:Alternate names: trypsinogen II

C:Species: Gallus gallus (chicken)

C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #ext\_change 22-Jun-1999

C:Accession: S55066; S72347

R:Yang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken trypsinogen gene family.

A:Reference number: S55065; MUID:95251611; PMID:7733885

A:Accession: S55066

A:Molecule type: mRNA

A:Residues: 1-248 <MAN>

A:Cross-references: EMBL:U15157; NID:9603906; PIDN:AAA79914.1; PID:9603907

A:Experimental source: clone 2-P29

A:Accession: S72347

A:Molecule type: DNA

A:Residues: 1-248 <MAN>

A:Cross-references: EMBL:U15157; NID:9603906; PIDN:AAA79914.1; PID:9603907

A:Experimental source: clone 2-P29

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-25/Domain: activation peptide #status predicted <APT>

F:26-248/Product: trypsin II #status predicted <MAT>

F:65, 109, 202/Active site: His, Asp, Ser #status predicted

Query Match 47.2%; Score 594; DB 2; Length 248;  
 Best Local Similarity 49.6%; Pred. No. 2.6e-45;  
 Matches 112; Conservative 35; Mismatches 73; Indels 6; Gaps 3;

QY 1 IIKGECKPHSQPMQALFEKTRILCGATLIPRMLTAAHCLKRYIVHLGQNLQKEE 60  
 Db 26 IYGGICPEHSPVYQVSL-NSGYHFCGSLINSQVLSAHCYKRIQVRLEGVNIDVE 84

QY 61 GGEOTRTATESPPHGFNNSLPNK-----DHRDMLVXKASPVSTWAVRPLTSSRCVTAGTS 120  
 Db 85 DSEVNVSSSVITRHPYSSITLNL---NDIMLIKLSAVEGADIPIALPSSCAKAGTE 140

QY 121 CLISGNGTSSTPOLRLPHLLRCANITIIHQKCNAYPGNITDVMCAVOEGGDSGCG 180  
 Db 141 CLISGNGTSLNGNYNPELLQCLNAPILSDQCEQYVPEIDITSNMTCVFLGSGDSCG 200

QY 181 DSGGPVLVNCOSLOGIISWGDPICATIRKPGYVTKYKXVDMIOETM 226  
 Db 201 DSGGPVLVNCOSLOGIISWGIG-CALKGYPGVYTKCNVYDMIOETI 245

RESULT 6

515686  
 tissue kallikrein (EC 3.4.21.35) precursor, renal - multimammate rat (Mastomys natalens)

C:Species: Mastomys natalensis

C:Date: 09-Jun-1994 #sequence\_revision 10-Nov-1995 #ext\_change 22-Jun-1999

C:Accession: I83227; S15686

R:Fahnestock, M.

DNA Cell Biol. 13, 293-300, 1994

A:Title: Characterization of kallikrein cDNAs from the African rodent Mastomys.

A:Reference number: I60208; MUID:94226702; PMID:7909667

A:Accession: I83227

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-263 <RES>

A:Cross-references: EMBL:X17352; NID:G55526; PIDN:CAA35232.1; PID:G55527  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase  
F:25-255/Domain: trypsin homology <TRY>  
F:65,121,215/Active site: His, Asp, Ser #status predicted

Query Match 47.0%; Score 591.5; DB 2; Length 263;  
Best Local Similarity 44.5%; Pred. No. 4,7e-45;  
Matches 106; Conservative 44; Mismatches 79; Indels 9; Gaps 2;

QY 1 IIGFECKPHSQPWAALFEKTRLLCGATILAPRWLTAHCLKPRYVHLCGHNLQKEE 60  
DB 25 IIGFENCKKSPQWPAVAYRPAQCGVLLDANWVLAHCYDKQVWLGRKRRFEDE 84  
QY 61 GCEQRTATSFPPHGFNNSLPNKDHRIIDLTVKMAAPSVITWVPLTLSSRCVTAGTS 112  
DB 85 PSAGHQLSKALPHRPFMSLNDHTRPHEDVSNLMLVRLKAPLIDVYKPIPLPT 144  
QY 113 RCTVAGTSLISGKSTGTS-SFQRLPHTLRCAANTTIEHOKCENAYPGNTTDMVCAVSQ 171  
DB 145 EEPVSGKCLASGMSGSTTPTEFEFYSHDLCVYLELLSNVCAKAHTEKVTDMLCAGEM 204  
QY 172 EGGDSGCGSGGLVNCQSLQGIISWGDPCLATRKPGVYTVCKYVDMIOETMKON 229  
DB 205 DGGKDTVCGSGFLICDGLVLTGTTSGPTPCALPNVPGIYTKLIERSWIKQVMANN 262

## RESULT 7

TRYPT  
trypsin (EC 3.4.21.4) II precursor - rat

N:Alternate names: trypsinogen II

C:Species: Rattus norvegicus (Norway rat)

C:Date: 05-Apr-1993 #sequence revision 30-Sep-1987 #text change 18-Jul-1997

A:Accession: A22657; A00949

F:Crailk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.

J. Biol. Chem. 259, 14255-14264, 1984

A:Title: Structure of two related rat pancreatic trypsin genes.

A:Reference number: A22657; MUID:85054880; PMID:6094547

A:Accession: A22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

R:MacDonald, R.J.; Steay, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00949

A:Molecule type: mRNA

A:Residues: 9-246 <MAC>

C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I mR

C:Genetics:

A:Insertions: 14/1; 67/2

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-23/Domain: activation peptide #status predicted <APR>

F:24-246/Product: trypsin II #status predicted <ENZ>

F:24-239/Domain: trypsin homology <TRY>

F:30-160/48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted

F:63,107,200/Active site: His, Asp, Ser #status predicted

F:73,77,80,85/Binding site: calcium (Glu, Asn, Val, Gln) #status predicted

Query Match

Best Local Similarity 47.0%; Score 591; DB 1; Length 246;

Matches 113; Conservative 32; Mismatches 78; Indels 6; Gaps 3;

QY 1 IIGFECKPHSQPWAALFEKTRLLCGATILAPRWLTAHCLKPRYVHLCGHNLQKEE 60  
DB 24 IIGFENCKKSPQWPAVAYRPAQCGVLLDANWVLAHCYDKQVWLGRKRRFEDE 84  
QY 61 GCEQRTATSFPPHGFNNSLPNKDHRIIDLTVKMAAPSVITWVPLTLSSRCVTAGTS 120  
DB 83 GDSGFNNAKILIHGPRDKRTLN---NDIMLIKSSPKLNARVATVALPSSCAPAGTQ 138

QY 121 CLISGWTSPQLPHTLRCAANTTIEHOKCENAYPGNTTDMVCAVSQVOEGKDCSQG 180  
DB 139 CLISGWTSLSSGVNEPDLQLDAPLPLPADCEASTPEKLTIDNVVCVGFLEGGKDCSQG 198  
QY 181 DSGGFLVNCQSLQGIISWGDPCLATRKPGVYTVCKYVDMIOETMKON 229  
DB 199 DSGGFLVNCQSLQGIISWGDPCLATRKPGVYTVCKYVDMIOETMKON 246

## RESULT 8

TRYPT  
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C:Date: 22-Nov-1993 #sequence revision 03-Aug-1995 #text change 22-Jun-1999

A:Accession: S66657; S31779

F:Male, R.; Lorenz, J.B.; Smalae, A.O.; Torrisen, K.R.

Eur. J. Biochem. 232, 677-685, 1995

A:Title: Molecular cloning and characterization of anionic and cationic variants of try

A:Reference number: S66657; MUID:96035908; PMID:7556223

A:Accession: S66657

A:Molecule type: mRNA

A:Residues: 1-238 <MAU>

A:Cross-references: EMBL:X70074; NID:G64387; PIDN:CAA49679.1; PID:G64388

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase

F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>

F:18-15/Domain: activation peptide #status predicted <APR>

F:16-238/Product: trypsin III #status predicted <MAU>

F:12-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted

F:55,99,192/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 46.7%; Score 588; DB 2; Length 238;

Matches 110; Conservative 35; Mismatches 78; Indels 6; Gaps 4;

QY 1 IIGFECKPHSQPWAALFEKTRLLCGATILAPRWLTAHCLKPRYVHLCGHNLQKEE 60  
DB 16 IIGFENCKKSPQWPAVAYRPAQCGVLLDANWVLAHCYDKQVWLGRKRRFEDE 84  
QY 61 GCEQRTATSFPPHGFNNSLPNKDHRIIDLTVKMAAPSVITWVPLTLSSRCVTAGTS 120  
DB 75 GCEQRTATSFPPHGFNNSLPNKDHRIIDLTVKMAAPSVITWVPLTLSSRCVTAGTS 130  
QY 121 CLISGWTSPQLPHTLRCAANTTIEHOKCENAYPGNTTDMVCAVSQVOEGKDCSQG 180  
DB 131 CLISGWTSLSSGVNEPDLQLDAPLPLPADCEASTPEKLTIDNVVCVGFLEGGKDCSQG 190  
QY 181 DSGGFLVNCQSLQGIISWGDPCLATRKPGVYTVCKYVDMIOETMKON 229  
DB 191 DSGGFLVNCQSLQGIISWGDPCLATRKPGVYTVCKYVDMIOETMKON 246

## RESULT 9

TRYPT  
trypsin (EC 3.4.21.4) I precursor - rat

N:Alternate names: trypsinogen I

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text change 24-Sep-1999

A:Accession: B22657; A00948

F:Crailk, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.

J. Biol. Chem. 259, 14255-14264, 1984

A:Title: Structure of two related rat pancreatic trypsin genes.

A:Reference number: A22657; MUID:85054880; PMID:6094547

A:Accession: B22657

A:Molecule type: DNA

A:Residues: 1-246 <CRA>

A:Cross-references: GB:J00778; NID:G206507; PIDN:AAA9518.1; PID:G206508

R:MacDonald, R.J.; Steay, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of

A:Reference number: A00948; MUID:82265624; PMID:6896710

A:Accession: A00948  
 A:Molecule type: mRNA  
 A:Residues: 1-246 <MC>  
 A:Cross-references: GB:U00778; NID:g206507; PIDN:AAA9518.1; PID:g206508  
 C:Genetics:  
 A:Introns: 14/1; 67/2; 152/1; 197/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:15-23/Domain: activation peptide #status predicted <AP>  
 F:24-246/Product: trypsin I #status predicted <ENZ>  
 F:24-239/Domain: trypsin I #status predicted <TRY>  
 F:30-107,48-66,132-233,139-206,171-185/Disulfide bonds: #status predicted  
 F:63,107,200/Active site: His, Asp, Ser #status predicted  
 F:73,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 46.7%; Score 587; DB 1; Length 246;  
 Best Local Similarity 48.5%; Pred. No. 1,1e-44;  
 Matches 111; Conservative 34; Mismatches 78; Indels 6; Gaps 3;

QY 1 IIKGFECRPHSQPQALFEKTRLLCGATLAPRWLLTAHCKRPYIVHLGQHNLOKEE 60  
 Db 24 IIVGYTPPEHSVPQVSL-NSGHFCGSLINDQWVSAHCKYKRIQVALGSHNVLE 82  
 QY 61 GCEQRTATSEFPHPGNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120  
 Db 83 GDEQFVNAKTIKHPNYSWTLN---NDIMLIKLSFVTLNARVAPVALPSACAPAGTQ 138  
 QY 121 CLISGMSSTSPQRLPHTLRCAANTIIIEHCKENAYPGNITDTWCASVQEGKDSVQEG 180  
 Db 139 CLISGMNTLISNGNNNDLLQCDAPVLSQADCEAAPGBITSMTCVGRLEEGKDSVQEG 198  
 QY 181 DSGGPLVNCNLSGIIISMGQDPCATRRPGVYTRKCVYVMIOETMKN 229  
 Db 199 DSGGPVNCNQLGIVSMGSG-CALPDNPGVYTRKVCNFCVMIOETMKN 246

RESULT 10  
 A34079  
 tissue kallikrein (EC 3.4.21.35) P1 precursor - rat  
 N:Alternate names: kallikrein-related proteinase K8  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 22-Jun-1999  
 C:Accession: A34079; S10700  
 R:Brady, J.M.; Wines, D.R.; MacDonald, R.J.  
 Biochemistry 28, 5203-5210, 1989  
 A:Title: Expression of two kallikrein gene family members in the rat prostate.  
 A:Reference number: A34079; MUID:89352606; PMID:2765531  
 A:Accession: A34079  
 A:Status: Preliminary  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-261 <BFA>  
 A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:9  
 R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.  
 FEBS Lett 265, 137-140, 1990  
 A:Title: Substrate specificity of two kallikrein family gene products isolated from the  
 A:Reference number: S10698; MUID:90306305; PMID:2194829  
 A:Accession: S10700  
 A:Molecule type: Protein  
 A:Residues: 25-43;112-138 <ELM>  
 A:Experimental source: submaxillary gland  
 A>Note: 125-Iys was also found  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:25-253/Domain: trypsin homology <TRY>  
 F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>  
 F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>  
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 46.5%; Score 585.5; DB 2; Length 261;  
 Best Local Similarity 44.5%; Pred. No. 1.6e-44;  
 Matches 105; Conservative 41; Mismatches 83; Indels 7; Gaps 1;

QY 1 IIKGFECRPHSQPQALFEKTRLLCGATLAPRWLLTAHCKRPYIVHLGQHNLOKEE 60  
 Db 25 IIGGFNCRKNSSQPMQVAAVYHFNPEQCGVLLHPSVAVITAAHCYSVNYOVWIGRNNLEDE 84  
 QY 61 GCEQRTATSEFPHPGNNSL-----PNKDRNDIMLVKMASPVSIWAVRPLTSSR 113  
 Db 85 PFAQRLVQSFPHPGFVLDIIKHTRKPGNDYSNDLMLHKTPADITDGKVIDLPTF 144  
 QY 114 CVTACTSCLISGMSSTSPQRLPHTLRCAANTIIIEHCKENAYPGNITDTWCASVQEG 173  
 Db 145 EKVYSTCLISGMSITLTKNEFPDDLQCVNIIHLSNEKCIKAYNDEVTDVWLCAEWDG 204  
 QY 174 GSDSQGSGGPLVNCNLSGIIISMGQDPCATRRPGVYTRKCVYVMIOETMKN 229  
 Db 205 GMDCKGSDGGPLICDVLQGITSMGMPGEPNRPVYTLKIFTSWKIKVKNEN 260

RESULT 11  
 B31136  
 tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat  
 N:Alternate names: glandular prokallikrein 3, submandibular  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 22-Jun-1999  
 C:Accession: B31136  
 R:Chen, Y.P.; Chao, J.; Chao, J.  
 Biochemistry 27, 7189-7196, 1988  
 A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.  
 A:Reference number: A31136; MUID:8908074; PMID:2845988  
 A:Accession: B31136  
 A:Molecule type: DNA  
 A:Residues: 1-259 <CHE>  
 A:Cross-references: GB:M19648; GB:J02837; NID:g205002; PIDN:AAA51640.1; PID:g205004  
 A>Note: The authors translated the codon GTC for residue 230 as Cys  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-259/Product: tissue prokallikrein 3, submandibular #status predicted <MAT>  
 F:25-251/Domain: trypsin homology <TRY>  
 F:63,118,211/Active site: His, Asp, Ser #status predicted

Query Match 46.2%; Score 581.5; DB 2; Length 259;  
 Best Local Similarity 44.5%; Pred. No. 3.6e-44;  
 Matches 105; Conservative 39; Mismatches 83; Indels 9; Gaps 2;

QY 1 IIKGFECRPHSQPQALFEKTRLLCGATLAPRWLLTAHCKRPYIVHLGQHNLOKEE 60  
 Db 25 VVGKCKCKNQPMQVAVI--NRYICGVLIDPMSVITAAHCYSHNVVLGRNNLPFDE 82  
 QY 61 GCEQRTATSEFPHPGNNSL-----NSLPKDRNDIMLVKMASPVSIWAVRPLTSSR 113  
 Db 83 PFAQRLVQSFPHPGFVLDIIKHTRKPGNDYSNDLMLHKTPADITDGKVIDLPTF 142  
 QY 114 CVTACTSCLISGMSSTSPQRLPHTLRCAANTIIIEHCKENAYPGNITDTWCASVQEG 173  
 Db 143 EKVYSTCLASGMSSTKLEWFPDDLQCVNIIHLSNEKCIKARTQMTDVMLCAGEIEG 202  
 QY 174 GSDSQGSGGPLVNCNLSGIIISMGQDPCATRRPGVYTRKCVYVMIOETMKN 229  
 Db 203 GMDCKGSDGGPLICDVLQGITSMGMPGEPNRPVYTLKIFTSWKIKVKNEN 258

RESULT 12  
 K09G  
 tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)  
 N:Alternate names: glandular kallikrein; kininogenin  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 24-Apr-1984 #sequence\_revision 31-Dec-1993 #text\_change 31-Mar-2000  
 C:Accession: A00938; A92895  
 R:Hirschschne, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, M.;  
 Adv. Exp. Med. Biol. 120, 245-260, 1979  
 A:Title: The primary structure of porcine glandular kallikreins.  
 A:Reference number: A90015





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QY 1 IIKGFCKPHSPQWQALFEKTRLLCGATLLIAPRWLLTAACLKPRYIVHLGQHNLOKEE 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 25 IVGFCKEKHSQPHVAVRYKNEYICGGVLLIDANWVLTAAHCYEEKSVLGGNNLYEE 84
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GCEQTRATESFPHPGFNNSL-----PNKDRNDIMLVKMASPVASITWAVRPLTISR 113
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 85 PSAQHRIVSKSFLLPGYRSHRNHRRHPEDYSDNDIMLRSLKPADITDVAKPLPTE 144
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 114 CVTAGTCLISGWSSTSPQLRPLTLRCANITITIEHQKCNAYPGNITDTWCASVQEG 173
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 145 EPKLIGSTCLASGWSSTTPFPQNAKDLQCVNLKLLPNEDCGKAHIEKVIDVMLCAEPTDG 204
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 174 GKSDCCGDSGAPLVNCSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 205 GKDTCKGDSGAPLIDCVLQGITSMGFTPGCEPKPGVYTKLTKFTSWIKDTMAKN 260
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

## RESULT 15

```
TRPCTR
trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
N:Contains: trypsinogen
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 31-Mar-2000
C/Accession: A90641; A90368; A00947
R/Charles, M.; Koverly, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
A/Title: Su le trypsinogene et la trypsine de porc.
A/Reference number: A90641
A/Accession: A90641
A/Molecule type: protein
A/Residues: 1-10 <CH>
R/Hermanson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
A/Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy
A/Reference number: A90368; MUID:73258692; PMID:4738933
A/Accession: A90368
A/Molecule type: protein
A/Residues: 9-231 <HER>
A/Note: at position 20, Ile and Val occur alternatively
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteolase; zym
F:1-231/Product: trypsinogen #status experimental <ZYM>
F:1-8/Domain: activation peptide #status experimental <APT>
F:9-231/Product: trypsin #status experimental <MAT>
F:9-224/Domain: trypsin homology <TRY>
F:15-145,13-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted
F:48,92,185/Active site: His, Asp, Ser #status predicted
F:60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
```

Query Match 45.9%; Score 577; DB 1; Length 231;

Best Local Similarity 47.8%; Pred. No. 7.9e-44; Matches 110; Conservative 35; Mismatches 77; Indels 8; Gaps 4;

```
QY 1 IIKGFCKPHSPQWQALFEKTRLLCGATLLIAPRWLLTAACLKPRYIVHLGQHNLOKEE 60
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 9 IVGFCKEKHSQPHVAVRYKNEYICGGVLLIDANWVLTAAHCYEEKSVLGGNNLYEE 67
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GCEQTRATESFPHPGFNNSL-----PNKDRNDIMLVKMASPVASITWAVRPLTISR 119
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 68 GNEQFINAAKIIITHPNFNGNTLD-----NDIMLIKISSPATINSRVATVSLPRSCAAAGT 122
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 SCHISGWSSTSPQLRPLTLRCANITITIEHQKCNAYPGNITDTWCASVQEGKDSQ 179
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 123 ECLISGWSSTSPQLRPLTLRCANITITIEHQKCNAYPGNITDTWCASVQEGKDSQ 182
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 180 GDSGGPLVNCOSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 229
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 183 GDSGGPLVNCOSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIOETMKN 231
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Search completed: June 22, 2004, 18:56:52  
Job time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 22, 2004, 18:48:51 ; Search time 17 Seconds  
(without alignments)  
701.416 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Sequence: 1 IIRGFECKPHSGPQWQALFE.....GVYTRVCKVYDVIQETMKNN 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	1	KLKB_HUMAN
2	736	58.5	250	1	KLKB_HUMAN
3	687	54.6	250	1	NRPN_RAT
4	684	54.4	250	1	NRPN_MOUSE
5	682	54.2	250	1	KLKB_HUMAN
6	681	54.1	250	1	KLKB_HUMAN
7	677.5	53.9	277	1	KLKB_HUMAN
8	644.5	51.2	293	1	KLKB_HUMAN
9	621	49.4	251	1	KLKB_HUMAN
10	606	48.2	248	1	KLKB_HUMAN
11	605.5	48.1	251	1	KLKB_HUMAN
12	600.5	47.7	251	1	KLKB_HUMAN
13	595.5	47.3	251	1	KLKB_HUMAN
14	594	47.2	248	1	KLKB_HUMAN
15	591.5	47.0	253	1	KLKB_HUMAN
16	591	47.0	253	1	KLKB_HUMAN
17	588	46.7	238	1	KLKB_HUMAN
18	587	46.7	246	1	KLKB_HUMAN
19	585.5	46.5	251	1	KLKB_HUMAN
20	581.5	46.2	259	1	KLKB_HUMAN
21	577.5	45.9	261	1	KLKB_HUMAN
22	577.5	45.9	261	1	KLKB_HUMAN
23	577	45.9	231	1	KLKB_HUMAN
24	577	45.9	244	1	KLKB_HUMAN
25	571	45.4	246	1	KLKB_HUMAN
26	570.5	45.3	246	1	KLKB_HUMAN
27	568	45.2	247	1	KLKB_HUMAN
28	567.5	45.0	259	1	KLKB_HUMAN
29	566.5	44.9	261	1	KLKB_HUMAN
30	564.5	44.9	261	1	KLKB_HUMAN
31	564	44.8	261	1	KLKB_HUMAN
32	564	44.8	261	1	KLKB_HUMAN
33	562	44.7	262	1	KLKB_HUMAN

## ALIGNMENTS

RESULT 1	ID	KLKB_HUMAN	STANDARD	PRT	250 AA.
AC	Q9UBX7	075837; Q9NS65;			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Kallikrein 11 precursor (EC 3.4.21.-) (Hypostasin) (Trypsin-like protease).				
DE	KLK11 OR PRSS20 OR TLSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RC	SEQUENCE FROM N.A. (ISOFORM 1).				
RP	TISSUE=Hippocampus;				
RX	MEDLINE=96438738; PubMed=9765601;				
RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiozaki S.;				
RT	cDNA cloning and expression of a novel serine protease, TLSP.				
RL	Biochim. Biophys. Acta 1399:225-228(1998).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Hippocampus, and Prostate;				
RX	MEDLINE=20329229; PubMed=10872828;				
RA	Mitsui S., Yanada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TLSP/hypostasin, (PRSS20), is expressed in the human brain and prostate."				
RL	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20130117; PubMed=10662548;				
RA	Yousef G.M., Scortolas A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family."				
RL	Genomics 63:88-96(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20510030; PubMed=11054574;				
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;				
RT	Mose P., Paepel B., Wang K.;				
RL	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."				
RL	Gene 257:119-130(2000).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RA	Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.;				
RA	Burthart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.;				
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.;				
RA	Dandaneu L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.;				
RA	Andreian T., Frankel M., Atlix C., Amico-Keller G., Coffield J.;				
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.;				
RA	Atellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.;				
RA	Olsen A.S., Carrano A.V.;				
RT	"Sequence analysis of chromosome 19q13.4."				

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;  
 RX MEDLINE=2338257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pears C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miallby S.J.,  
 RA Bosak A.S., McGowan P.J., McKernan K.J., Malek J.A., Guntaratne P.H.,  
 RA Richards S., Mowley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Possible multifunctional protease. Efficiently cleaves  
 bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and  
 CC weakly cleaves other substrates for kallikrein and trypsin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9UBX7-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9UBX7-2; Sequence=VSP\_005402;  
 CC -1- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform  
 CC 1 is expressed preferentially in brain, isoform 2 in prostate.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 CC -----  
 DR EMBL: ABO12917; BAA33404.1; ALT\_INIT.  
 DR EMBL: ABO13730; BAA8713.1; -  
 DR EMBL: ABO41036; BAA96797.1; -  
 DR EMBL: AF164623; AAD47815.1; -  
 DR EMBL: AF243527; AAG33564.1; -  
 DR EMBL: AC011473; AAG3257.1; -  
 DR EMBL: BC022068; AAG22068.1; -  
 DR HSSP: P00763; IDPO.  
 DR MEROPS: S01.257; -  
 DR Gene: HGNC:6359; KLK11.  
 DR MTX: 60434; -  
 DR GO: GO:0008236; P:serine-type peptidase activity; TMS.  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYP\_SPC\_1.  
 DR PROSITE: PS0240; TRYPSEIN\_DOM\_1.  
 DR PROSITE: PS00134; TRYPSEIN\_HIS\_1.  
 DR PROSITE: PS00135; TRYPSEIN\_SER\_1.  
 KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;  
 KW Alternative splicing.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 21 ACTIVATION PEPTIDE (POTENTIAL).  
 FT CHAIN 22 250 KALLIKREIN 11.

FT ACT\_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISTLFD 28 163 BY SIMILARITY.  
 FT DISTLFD 47 63 BY SIMILARITY.  
 FT DISTLFD 135 237 BY SIMILARITY.  
 FT DISTLFD 142 209 BY SIMILARITY.  
 FT DISTLFD 174 188 BY SIMILARITY.  
 FT DISTLFD 199 224 BY SIMILARITY.  
 FT CAROHD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROHD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 1 M -> MORELWRMKSNGGLTAAPKAPARSSPLQAM  
 (in isoform 2).  
 FT /Frid=VSP\_005402.  
 SQ SEQUENCE 250 AA; 2746 MW; 192D910B8C0C7A56 CRC64;  
 Query Match 100.0%; Score 1258; DB 1; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-109;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IIKGFCKPHSQPQALFEKTRLLCGATLTAAPWLTAAHCLKPRYIVHGLGNLQKEE 60  
 DB 22 IIKGFCKPHSQPQALFEKTRLLCGATLTAAPWLTAAHCLKPRYIVHGLGNLQKEE 81  
 QY 61 GCEQRTATSEFPHPGNNSLPNKDRNDLVMASPVSIWAVRPLTSSRCVTRGTS 120  
 DB 82 GCEQRTATSEFPHPGNNSLPNKDRNDLVMASPVSIWAVRPLTSSRCVTRGTS 141  
 QY 121 CLISWGSTSSPOLRLPHTLRCAVITLIEHOKCNAPVAGITPDMMVCAVQEGGKSCOG 180  
 DB 142 CLISWGSTSSPOLRLPHTLRCAVITLIEHOKCNAPVAGITPDMMVCAVQEGGKSCOG 201  
 QY 181 DSGGFLVGNQSLQGIISWGDPICATITRKPGVYTKVCKYVMIGETMKN 229  
 DB 202 DSGGFLVGNQSLQGIISWGDPICATITRKPGVYTKVCKYVMIGETMKN 250  
 RESULT 2  
 ID KUK9 HUMAN STANDARD; PRT; 250 AA.  
 AC Q9UKQ9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-  
 DE L3).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBTaxid=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20118156; PubMed=10652563;  
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
 RT "Identification of novel human kallikrein-like genes on chromosome  
 RT 19q13.3-q13.4.";  
 RT Anticancer Res. 19:2843-2852(1999).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20247258; PubMed=10783266;  
 RA Yousef G.M., Diamandis E.P.;  
 RT "The expanded human kallikrein gene family: locus characterization and  
 RT molecular cloning of a new member, KLK-L3.";  
 RT Genomics 65:184-194(2000).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2051030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Mose P., Paepel B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene

RT cluster located in chromosome 19q13 region."  
 RL Gene 257:119-130(2000).  
 (4)  
 RP SEQUENCE FROM N.A.  
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viewnathan V.,  
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Carnes J.,  
 RA Dangeman L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Frankel M., Altix C., Amico-Keller G., Coefield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of chromosome 19q13.4";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal  
 CC cord.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC -----  
 DR EMBL, AF135026; AAD26427.2; -;  
 DR EMBL, AF243527; AAG33562.1; -;  
 DR EMBL, AC011473; AAG23255.1; -;  
 DR HSSP, P00763; IDPO.  
 DR MEROPS, S01.307; -;  
 DR Gene: HGNC:6370; KLR9.  
 DR MIM, 605504; -;  
 DR GO, GO:0005576; C:extracellular; NAS.  
 DR GO, GO:0004522; F:serine-type endopeptidase activity; NAS.  
 DR GO, GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS, PRO0722; CHYMOTRYPSIN.  
 DR SMART, SM0020; TRYP\_SPC; 1.  
 DR PROSITE, PS50240; TRYP\_SIN\_DOM; 1.  
 DR PROSITE, PS00134; TRYP\_SIN\_HIS; 1.  
 DR PROSITE, PS00135; TRYP\_SIN\_SER; 1.  
 KM Hydroxylase, Serine protease, Glycoprotein, Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 250  
 FT ACT\_SITE 63 63 KALLIKREIN 9.  
 FT ACT\_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 29 164 BY SIMILARITY.  
 FT DISULFID 48 64 BY SIMILARITY.  
 FT DISULFID 136 238 BY SIMILARITY.  
 FT DISULFID 143 210 BY SIMILARITY.  
 FT DISULFID 175 189 BY SIMILARITY.  
 FT DISULFID 200 225 BY SIMILARITY.  
 FT DISULFID 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 211 211 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SO SEQUENCE 250 AA; 27512 MW; F2785245B063B88 CRC64;  
 Query Match 58.5%; Score 736; DB 1; Length 250;  
 Best Local Similarity 58.7%; Pred. No. 7,6e-61;  
 Matches 111; Conservative 35; Mismatches 57; Indels 0; Gaps 0;  
 QY 6 ECKENHOPMAALFEKTRLLCGATLAPRWLLPAACIKPRIVHICGNLCKECCBCT 65  
 DB 28 ECKRNPQWAGLPHLRFCGATLISDRWLLPAACIKRPRVYVWRIGEHLMKWSBBDL 87  
 QY 66 RYATESPFBPGFNNSLPNKDRNDIMLVKXASPVSLTMAVRPLTLSSRCVTAGTSLIG 125

DB 88 FRVTDFFPHFPGFNDSANDNDIMLRPRQARLSRPAYQPLNTSQTQVSPMGCLISG 147  
 QY 126 WGSTSSPQLRLPHTRCANITIIHOKCENAYPGNITDTWVCASVQEGKDSCGDSGCP 185  
 DB 148 WGAVSSPAPLFPVTLQCANISILENKLCHMAVYPGHISDSMLCAGLWEGGRSGSCGDSGCP 207  
 QY 186 LVNQSLOGILISWGDDPCAIRKRGVYTKYCKVDWIOETMKN 228  
 DB 208 LVNGLTAGVSGAEPSCRRPRRAYVTSVCHYLDWIQETWEN 250  
 RESULT 3  
 NRPN\_RAT  
 ID NRPN\_RAT STANDARD; PRT; 260 AA.  
 AC 088780;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropein precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine  
 DE protease 1).  
 GN KLR9 OR PRSS19 OR NRPN OR BSP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Brain;  
 RC MEDLINE=96389725; PubMed=9722524;  
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;  
 RT "Serine proteases in rodent hippocampus."  
 RL J. Biol. Chem. 273:23004-23011(1998).  
 CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and  
 CC hippocampal plasticity. Has a strong proteolytic activity against  
 CC fibronectin (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- TISSUE SPECIFICITY: Restricted to hippocampus.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, AJ005641; CA06643.1; -;  
 DR HSSP, Q61955; INEW.  
 DR MEROPS, S01.244; -;  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS, PRO0722; CHYMOTRYPSIN.  
 DR SMART, SM0020; TRYP\_SPC; 1.  
 DR PROSITE, PS50240; TRYP\_SIN\_DOM; 1.  
 DR PROSITE, PS00134; TRYP\_SIN\_HIS; 1.  
 DR PROSITE, PS00135; TRYP\_SIN\_SER; 1.  
 KM Hydroxylase, Serine protease, Glycoprotein, Zymogen, Signal.  
 FT SIGNAL 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73 NEUROPSIN.  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 39 173 BY SIMILARITY.  
 FT DISULFID 58 74 BY SIMILARITY.  
 FT DISULFID 145 246 BY SIMILARITY.  
 FT DISULFID 152 218 BY SIMILARITY.  
 FT DISULFID 184 198 BY SIMILARITY.  
 FT DISULFID 208 233 BY SIMILARITY.

FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 260 AA; 28510 MW, 58DF4F0602A0B7F5 CRC64;  
 Query Match 54.6%; Score 687; DB 1; Length 260;  
 Best Local Similarity 53.5%; Pred. No. 2, 7e-56;  
 Matches 121; Conservative 35; Mismatches 68; Indels 2; Gaps 2;

QY 1 IIRGFECKPSPQWQALFEKTRLLCGATLIRPMLLTAAHCLIPRYVILGQHNLOKEE 60  
 DB 33 ILGGECKPSPQWQALFEKTRLLCGATLIRPMLLTAAHCLIPRYVILGQHNLOKEE 92  
 QY 61 GCEQTRATESPPHGFENSLFNKDRNDIMLVKASPSVITWAPRLTSLRCYTAGIS 120  
 DB 93 EPEQEIQVARSIOHPGFENSLFNKDRNDIMLVKASPSVITWAPRLTSLRCYTAGIS 151  
 QY 121 CLISGWSSTSPQLRLPHTLRGANTITIEHOKCENAYPGNITPDVWCAVSGKDCOG 180  
 DB 152 CLISGWSSTSPQLRLPHTLRGANTITIEHOKCENAYPGNITPDVWCAVSGKDCOG 210  
 QY 181 DSGGPIVNCNQLGGIISWGDPICATIRKPGVYTRKCYVDMIGETM 226  
 DB 211 DSGGPIVNCNQLGGIISWGDPICATIRKPGVYTRKCYVDMIGETM 256

RESULT 4  
 NRPN MOUSE STANDARD; PRT; 260 AA.  
 ID NRPN MOUSE  
 AC 061955;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).  
 GN K18 OR PRS19 OR NRPN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Hippocampus;  
 RX MEDLINE=95348817; PubMed=7623137;  
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,  
 RA Ito J., Nishino H., Almqvist S., Kiyama H., Shiozaka S.;  
 RT "Expression and activity-dependent changes of a novel limbic-serine  
 RT protease gene in the hippocampus."  
 RU J. Neurosci. 15:5088-5097(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yoshida S., Hirata A., Inoue N., Shiozaka S.;  
 RT "Cloning and assignment of mouse neuropilin gene, Prs19 to chromosome  
 RT 7B4."  
 RU Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusik A., Farmer A.A., Rubin G.W., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Carninci P., Pange C.,  
 RA Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Pange C.,  
 RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mallat S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren J.J., Lu X., Gibbs R.A.,  
 RA Fealy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schenck A., Schein J.E., Jones S.T.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [4]  
 RP SEQUENCE OF N-TERMINUS AND CHARACTERIZATION.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=98225202; PubMed=9556608;  
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,  
 RA Shiozaka S., Midorikawa R., Kamachi T., Kawabe A., Shiozaka S.;  
 RT "Characterization of recombinant and brain neuropilin, a  
 RT plasticity-related serine protease."  
 RU J. Biol. Chem. 273:11189-11196(1998).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.  
 RC TISSUE=Hippocampus;  
 RX MEDLINE=99134351; PubMed=9933620;  
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,  
 RA Shiozaka S., Hakoshima T.;  
 RT "Crystal structure of neuropilin, a hippocampal protease involved in  
 RT kindling epileptogenesis."  
 RU J. Biol. Chem. 274:4220-4224(1999).  
 RL [6]  
 CC -1 FUNCTION: Suggested to be involved in kindling epileptogenesis and  
 CC hippocampal plasticity. Has a strong proteolytic activity against  
 CC fibronectin.  
 CC -1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-  
 CC -1 ENZYME REGULATION: Strongly inhibited by diisopropyl  
 CC fluorophosphate, leupeptin and (4-aminophenyl)metanesulfonyl 1-  
 CC fluoride.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: Expressed specifically in the limbic system of  
 CC mouse brain and is localized at highest concentration in pyramidal  
 CC neurons of the hippocampal CA1-3 subfields.  
 CC -1 MASS SPECTROMETRY: MS=26613; METHOD=MALDI; RANGE=29-260.  
 CC -1 MASS SPECTROMETRY: MS=26229; METHOD=MALDI; RANGE=33-260.  
 CC -1 SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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 CC -----  
 DR EMBL: D30785; BAA06451.1; -  
 DR EMBL: AB032202; BAA92435.1; -  
 DR EMBL: BC055895; AAH55895.1; -  
 DR PIR: I56559; I56559.  
 DR PDB: INPM; 23-MAR-99.  
 DR MEROPS: S01.244; -  
 DR MGD: MGI:892018; K1x8.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin.1.  
 DR PRINTS: PR00722; CHYOTRYPsin.  
 DR SMART: SM00020; TRYP\_SPC; 1.  
 DR PROSITE: PS0240; TRYPsin DOM; 1.  
 DR PROSITE: PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE: PS00135; TRYPsin\_SER; 1.  
 KM Hydrolyse: Serine protease; Zymogen; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73  
 FT ACT\_SITE 120 120  
 FT ACT\_SITE 212 212  
 FT DISULFID 39 173  
 FT DISULFID 58 74  
 FT DISULFID 145 246  
 FT DISULFID 152 218  
 FT DISULFID 164 198

FT DISULFID 208 233  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT STRAND 34 34  
 FT STRAND 37 38  
 FT TURN 41 42  
 FT TURN 45 46  
 FT STRAND 47 52  
 FT TURN 53 54  
 FT STRAND 55 64  
 FT TURN 65 66  
 FT STRAND 67 70  
 FT HELIX 72 74  
 FT STRAND 80 83  
 FT STRAND 87 87  
 FT TURN 88 89  
 FT STRAND 96 98  
 FT STRAND 100 105  
 FT TURN 107 108  
 FT TURN 114 115  
 FT TURN 118 119  
 FT STRAND 122 126  
 FT STRAND 140 141  
 FT TURN 148 149  
 FT STRAND 151 156  
 FT STRAND 170 170  
 FT STRAND 172 178  
 FT HELIX 181 187  
 FT TURN 189 193  
 FT TURN 194 195  
 FT STRAND 196 200  
 FT TURN 202 203  
 FT STRAND 206 206  
 FT TURN 209 210  
 FT TURN 212 213  
 FT STRAND 215 218  
 FT TURN 219 220  
 FT STRAND 221 228  
 FT STRAND 235 235  
 FT TURN 236 237  
 FT STRAND 238 238  
 FT STRAND 240 244  
 FT HELIX 245 256  
 SEQENCE 260 AA; 28523 MW; BE5FE6BE37CD60E CRC64;

Query Match 54.4%; Score 684; DB 1; Length 260;  
 Best Local Similarity 53.1%; Pred. No. 5.1e-56;  
 Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IITGFECKRPSQWQALFEKTRLLCGATLIARMLITAAHCKPKYIVHLGQHNQKE 60  
 DB 33 ILEGRECIPIPSQWQALFQGERLIGGVIVGDRWVLTAAHCKKQKYVRLGPHSLQSD 92  
 QY 61 GCEQRTATSPFPHGPNLPMKDHNDIMLVKMAPSVITAVRPLTISRCAVAGTS 120  
 DB 93 QPPEQIVQASIQHPCYNNNP-EDSHDMLIRLQNSANLSDKXKPVQLANICPRVQK 151  
 QY 121 CLISGWSGTSPPQLRPLHTLRCAKITIIEHOKENAVPGNITDTWYCASVQEGKDSQCG 180  
 DB 152 CIISGWTIVSPQENFNTINCAEVKIVSQNKCEKAPVPGITEGWYCACG-SSNGADTCOG 210  
 QY 181 DSGGPLVNCQSLQGITSMGODPCATIRKPGVYTKCKYVDWIGETMKN 228  
 DB 211 DSGGPLVNCQSLQGITSMGSDPGCKRPEKPGVYTKICKYITWIKTMDN 258

RESULT 5  
 KLFK HUMAN STANDARD; PRT; 256 AA.  
 AC Q9H2R5; O15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).

GN KLFK15.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RA PubMed=11010966;  
 RA Youssef G.M., Scortlas A., Jung K., Ashworth L.K., Diamandis E.P.;  
 RT "Molecular cloning of the human Kallikrein 15 gene (KLFK15). Up-  
 regulation in prostate cancer.";  
 RL J. Biol. Chem. 276:53-61(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepke B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [3]  
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94289486; PubMed=8018728;  
 RX Dhanich M.E., Spiess M.;  
 RT "A novel serine proteinase-like sequence from human brain.";  
 RL Biochim. Biophys. Acta 1218:225-228(1994).  
 CC -1- FUNCTION: Protease whose physiological substrate is not yet known.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q9H2R5-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9H2R5-2; Sequence=VSP\_005405;  
 CC Name=3;  
 CC IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407;  
 CC Name=4;  
 CC IsoId=Q9H2R5-4; Sequence=VSP\_005404;  
 CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also  
 expressed in the prostate, salivary, and adrenal glands and in the  
 colon testis and kidney.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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 CC -----  
 CC EMBL AF242195; AAG09469.1; -  
 CC EMBL AF242195; AAG09470.1; -  
 CC EMBL AF242195; AAG09471.1; -  
 CC EMBL AF242195; AAG09472.1; -  
 CC EMBL AF243527; AAG33354.1; -  
 CC EMBL X75363; CA531445.1; ALT\_SEQ.  
 CC HSSP; P00763; IDPO.  
 CC MEROPS; S01.081; -  
 CC GO; GO:0005576; C:extracellular; NAS.  
 CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
 CC GO; GO:0006506; F:proteolysis and peptidolysis; NAS.  
 CC InterPro; IPR009003; Cys\_Ser\_Trypsin.  
 CC InterPro; IPR001254; Peptidase\_S1.  
 CC Pfam; PF00089; trypsin\_1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC PROSITE; PS50240; TRYPSIN\_DOM. 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS. 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NEG.  
 CC Hydrolase; Serine protease; Glycoprotein; signal; zymogen;  
 CC Alternative splicing.

```

FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 21 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 22 256 KALLIKREIN 15.
FT ACT_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 106 106 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 209 209 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 122 206 Missing (in isoform 4).
FT VARSPIC 122 256 /FTid=VSP_005404.
FT VARSPIC 161 161 /FTid=VSP_005405.
FT VARSPIC 161 161 V -> G (in isoform 3).
FT VARSPIC 162 256 /FTid=VSP_005406.
FT VARSPIC 162 256 Missing (in isoform 3).
FT CONFLICT 147 160 SHNEPAGSPRSO -> PLSSP (IN REF. 2).
FT SEQUENCE 256 AA; 28087 MM; B5EBF8D6022786B5 CRG4;

Query Match 54.2%; Score 682; DB 1; Length 256;
Best Local Similarity 51.9%; Pred. No. 7.6e-56;
Matches 124; Conservative 36; Mismatches 65; Indels 14; Gaps 3;

QY 1 IITGFEKPSQPMQALFEKTLTGATLIRWILTAHCLKRYIVHIGQHNQKE 60
DB 22 LLEGECPHSPQWQVALYERGFNCASLISPHWLSAHCQSRFRVRLGSHNRKD 81
QY 61 GCEQTRATESFPHGFNNSLPNKDRNDIMLVKASPVSIYAVPLTSSRCVATGS 120
DB 82 GPDLARTTSVIVHPRE---ARSHRNDIMLRVLQPARLNQVAPVLPFCRHPGBA 137
QY 121 CLISGWGSTS-----SP--QLRLPHTRCANITITHEKQENAYFENIDTWCASV 170
DB 138 CWSGVMGLVSHNEPRTAGSPRSQVSLPDLTHCANISIIISPTCDKSPRLNTWYCA 197
QY 171 QEGSKDSQCGDSGAPLVCCNCSLOGIISWGDPCAIRKPGVYKVKCYDVIQETMK 229
DB 198 EGRGABCEGDSGGLVCGSILGIVSMGVPCDNTTKGVYIKVCHYLEMIREMKRN 256

RESULT 6
KLK8 HUMAN STANDARD; PRT; 260 AA.
ID 060259; Q9HCB3; Q9HIL9; Q9U047;
AC 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neutropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
DE protease TAD3-14) (Tumor-associated differentially expressed gene-14
DE protein).
GN KLK8 OR PRSS19 OR TAD314 OR NRPN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=86372070; PubMed=9714609;
RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
RT "Sequence analysis and expression of human neutropsin cDNA and gene.";
RL Gene 213:9-16(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=99203457; PubMed=101029950;
RA Mitsui S., Tsunoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
RT "A novel form of human neutropsin, a brain-related serine protease, is
RT generated by alternative splicing and is expressed preferentially in
RT human adult brain.";
RL Eur. J. Biochem. 260:627-634(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).

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RC TISSUE=Ovary;
RX MEDLINE=99413504; PubMed=10485494;
RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Paroley T.H.,
RA O'Brien T.J.;
RT "Cloning of tumor-associated differentially expressed gene-14, a novel
RT serine protease overexpressed by ovarian carcinoma.";
RL Cancer Res. 59:4433-4439(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;
RT "Molecular cloning and characterization of a novel serine protease,
RT ovasin, a potential molecular marker for ovarian carcinoma.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paeger B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [6]
RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burthart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garne J.,
RA Darganau L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andrease T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP FUNCTION: Suggested to be involved in kindling epileptogenesis and
RP hippocampal plasticity.
RN [8]
RP CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
RN [9]
RP SUBCELLULAR LOCATION: Secreted.
RN [10]
RP ALTERNATIVE PRODUCTS:
RN [11]
RP Event-Alternative splicing; Named isoforms=2;
RN [12]
RP Name=1;
RN [13]
RP IsoId=060259-1; Sequence=Displayed;
RN [14]
RP Name=2;
RN [15]
RP IsoId=060259-2; Sequence=VSP_005401;
RN [16]
RP TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the
RP pancreas while isoform 2 is expressed in adult brain and
RP hippocampus. Both forms are also found in fetal brain and
RP placenta. Not detected in kidney, spleen, liver and lung.
RN [17]
RP SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
RN [18]
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RP or send an email to license@isb-sib.ch).
RN [19]
RP EMBL: AB009849; BAA2673.1; -
RN [20]
RP EMBL: AB012761; BAA2676.1; -
RN [21]
RP EMBL: AB012761; BAA2676.1; -
RN [22]
RP EMBL: AB008390; BAA2685.1; -
RN [23]
RP EMBL: AB008390; BAA2685.1; -
RN [24]
RP EMBL: AB008927; BAA2666.1; -
RN [25]
RP EMBL: AB008927; BAA2666.1; -
RN [26]
RP EMBL: AF095742; AAD25979.1; -
RN [27]
RP EMBL: AF095742; AAD25979.1; -
RN [28]
RP EMBL: AF243527; AAG33361.1; -
RN [29]
RP EMBL: AF243527; AAG33361.1; -
RN [30]
RP EMBL: AC011473; AAG33254.1; -
RN [31]
RP HSSP: O61955; INPW.
RN [32]
RP MEROPS: S01.244; -
RN [33]
RP Genew: HGNC:6369; KLK8.
RN [34]
RP MIM: 605644; -
RN [35]
RP GO: GO:0008236; F:serine-type peptidase activity; TAS.
RN [36]
RP GO: GO:0007399; P:neurogenesis; TAS.

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RA Lamerdi J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias U., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Dangman L., Eriksson K., Christensen M., Georgescu A., Aylit J., Liu S.,
RA Andrade T., Trillerkhim M., Attix C., Amico-Keller G., Coelfield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Ariellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RL "Sequence analysis of chromosome 19p13.4 ";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE=uterus;
RA Ansoyge M., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and
CC salivary gland.
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF135024; AAD6425.2; -.
CC EMBL: AC01473; AAG23255.1; -.
CC EMBL: AL050220; CAB4320.1; ALT_INT1.
CC HSSP: P00763; IDPO.
CC MEROPS: S01.306; -.
CC Genew: HGNC:6361; KLK13.
CC MIM: 605505; -.
CC GO: GO:0005576; C:extracellular; NAS.
CC GO: GO:0004252; F:setine-type endopeptidase activity; NAS.
CC GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
CC InterPro: IPR009003; Cys_Ser_trypsin.
CC InterPro: IPR001254; Peptidase_S1.
CC InterPro: IPR001314; Peptidase_S1A.
CC Pfam: PF00089; trypsin; 1.
CC PRINTS: PRO0722; CHYMOTRYPSIN.
CC SMART: SM0020; TRYPSIN_DOM; 1.
CC PROSITE: PS00240; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC K01 Hydroxylase; Serine protease; Glycoprotein; Signal.
FT CHAIN 1 16 POTENTIAL.
FT ACT_SITE 17 277 KALLIKREIN_13.
FT ACT_SITE 76 76 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHANGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 42 178 BY SIMILARITY.
FT DISULFID 61 77 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT DISULFID 214 239 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 170 180 UNRELIABLE -> GMPHFWPEAP (IN REF. 3).
FT CONFLICT 277 AA; 30570 MW; BA8A5E8DCFB5D542 CRC64;
SQ SEQUENCE 277 AA; 30570 MW;
Query Match 53.9%; Score 677.5; DB 1; Length 277;
Best Local Similarity 53.3%; Pred.No. 2.2e-55;
Matches 120; Conservative 41; Mismatches 63; Indels 1; Gaps 1.
Oy 4 GFECKPHSQPQALAEFEKTKLLCATLTIAAPRWLTIAHCLKPRVYIHLGQHNLOKEGCE 63
Db 39 GVTCPFHSPQWQALVYGRLLGCGVLYVHKRWLTIAHCLKEGLKYLDGHALGRVEAGE 98
Oy 64 QYRIATSESPHGFENNSLPKQKHNDIMLVKMASPVISITAAVAPFLLS-SRCVTAQISTL 122

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Db 99 QVEEVHSDIPHEVRSPTLHNDHDMIELQSPVOLNGYIOTLPLSHNNRITPTGTCR 158  
 QY 123 ISGNGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGKDSQCQS 182  
 Db 159 VSGMGTTSPQVNVKTLQCANIQLSDECRQVYFGKTDNMLCAGTEGGKDSCEGDS 218  
 QY 183 GGPVNCQSLQGIISWGQPCATIRKPGVYTKCKYVDIMQETMK 227  
 Db 219 GGPVNCNRLTYGIVSWGDPFCQGPDPGRGVYTRVSRVYLWIRETR 263

RESULT 8  
 KLS\_HUMAN STANDARD; PRT; 293 AA.  
 ID KLS\_HUMAN  
 AC Q9Y337; Q9H8G8;  
 DT 16-OCT-2001 (Ref. 40, Created)  
 DT 16-OCT-2001 (Ref. 40, Last sequence update)  
 DT 15-MAR-2004 (Ref. 43, Last annotation update)  
 DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)  
 DB (Kallikrein-like protein 2) (KLR-L2).  
 GN KLS OR SCTE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 ON NCBI\_TaxId=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stratum corneum;  
 RX MEDLINE=99445563; PubMed=10514469;  
 RA Bratseand M., Egeldrud T.;  
 RT "Purification, molecular cloning, and expression of a human stratum  
 RT corneum trypsin-like serine protease with possible function in  
 RT desquamation.";  
 RL J. Biol. Chem. 274:30033-30040(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20118156; PubMed=10652563;  
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
 RT "Identification of novel human kallikrein-like genes on chromosome  
 RT 19q13.3-q13.4.";  
 RL Anticancer Res. 19:2843-2852(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McGuig J.,  
 RA Moss P., Paepker B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Satchell M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pae E.S.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalando D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smolus D.E.,  
 RA Scherch A., Schein U.E., Jones S.U.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC - FUNCTION: May be involved in desquamation.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.  
 CC - SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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DR EMBL AF158768; AAF03101.1; -  
 DR EMBL AF155028; AAD26429.1; -  
 DR EMBL AF243527; AAG33358.1; -  
 DR EMBL BC008036; AAB08036.1; -  
 DR HSRP; P00763; IDPO.  
 DR HSRP; S01.017; -  
 DR Genew; HGNC:6366; KLS.  
 DR MIM; 605643; -  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
 DR GO; GO:0008544; P:epidermal differentiation; TAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase S1.  
 DR InterPro: IPR001314; Peptidase S1A.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS02040; TRYPsin DOM; 1.  
 DR PROSITE; PS00344; TRYPsin HIS; 1.  
 DR PROSITE; PS00135; TRYPsin\_Ser; 1.  
 KM Hydrolyse; Serine protease; Glycoprotein; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 293  
 FT ACT\_SITE 108 198 KALLIKREIN 5.  
 FT ACT\_SITE 153 153 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 73 206 BY SIMILARITY.  
 FT DISULFID 93 109 BY SIMILARITY.  
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 FT DISULFID 185 251 BY SIMILARITY.  
 FT DISULFID 217 231 BY SIMILARITY.  
 FT DISULFID 241 266 BY SIMILARITY.  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 25 56 MISSING (IN REF. 3).  
 SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 51.2%; Score 644.5; DB 1; Length 293;  
 Best Local Similarity 50.6%; Pred. No. 2.6e-52;  
 Matches 117; Conservative 40; Mismatches 67; Indels 7; Gaps 4;

QY 1 IIKSECKPHSQPQAA-LFEKRLTLCGATLAPRWLTAAHCKIPRYIYHCOHNIQK-58  
 Db 67 IINSDDCMHQPOQALLLRPNQYCGAVLVHPQWLLTAHCRKKYFRLSHYISLSPV 126  
 QY 59 EEGCEQRTAIESPHGFGNNSLPNKDRDIMLVKASVSTWVAEPLTSSRCTAG 118  
 Db 127 YESQQMFQGVKSLPHGYS---HPGSHNDMLITKRRIRPTKQDPVNVSSHCPSAG 182  
 QY 119 TSLISGNGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGKDSQC 178  
 Db 183 TKLVSGMGTTSPQVNVKTLQCANIQLSDECRQVYFGKTDNMLCAGTEGGKDSCEGDS 241  
 QY 179 QGDSGGPVNCQSLQGIISWGQPCATIRKPGVYTKCKYVDIMQETMKRN 229  
 Db 242 QGDSGGPVNCQSLQGIISWGQPCAPRPNRGVYTNLCFTKTIQETIQAN 292

RESULT 9  
KLC6 HUMAN STANDARD; PRT; 251 AA.  
ID KLC6 HUMAN  
AC Q9P063;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6) (KLC14)  
GN KLC14 OR KLC16.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yousef G.M., Diamandis E.P.;  
RT "Molecular characterization, mapping, and tissue expression of KLC16, a hormonally regulated kallikrein-like gene."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.  
RA MEDLINE=21250937; PubMed=11352573;  
RA Hooper U.D., Bui L.T., Rae P.K., Harvey T.J., Myers S.A.,  
RA Ashworth L.K., Clements J.A.;  
RT "Identification and characterization of KLC14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."  
RL Genomics 73:117-122 (2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Lamedin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
RA Burkhart-Schulze K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,  
RA Dangnan L., Ecker A., Christensen M., Georgescu A., Avila J., Liu S.,  
RA Andrade T., Trakheim M., Attix C., Amico-Keller G., Coefield J.,  
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
RA Avellano A., Sanders C., Ow D., Nolan M., Trong S., Kodayashi A.,  
RA Olsen A.G., Carraro A.V.;  
RT "Sequence analysis of chromosome 19q13.4."  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP TISSUE SPECIFICITY.  
RA MEDLINE=20545474; PubMed=10969073;  
RA Harvey T.J., Hooper U.D., Myers S.A., Stephenson S.A., Ashworth L.K.,  
RA Clements J.A.;  
RT "Tissue-specific expression patterns and fine mapping of the human kallikrein (KLC) locus on proximal 19q13.4."  
RL J Biol. Chem. 275:37397-37406 (2000).  
RN [5]  
RP SUBCELLULAR LOCATION: Secreted (Probable).  
CC -||- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.  
CC -||- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
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CC  
EMBL, AF161231; AAD50773.2;  
EMBL, AF283669; AAK48523.1;  
EMBL, AF283670; AAK48524.1;  
EMBL, AC011473; AAG3260.1;  
HSSP; P00763; IDPO.  
MEROPS; S01.029;  
Genew; HGNC:6362; KLC14.  
MIM; 606135;  
GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; trypsin\_1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYD\_SPC; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KM Hydrolyase; Serine protease; Signal; Zymogen.  
FT SIGNAL 1 18  
FT PROPEP 19 24  
FT CHAIN 25 251  
FT ACT\_SITE 67 67 KALLIKREIN 14.  
FT ACT\_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT DISULFID 31 164 BY SIMILARITY.  
FT DISULFID 52 68 BY SIMILARITY.  
FT DISULFID 143 210 BY SIMILARITY.  
FT DISULFID 175 189 BY SIMILARITY.  
FT DISULFID 200 225 BY SIMILARITY.  
SQ SEQUENCE 251 AA; 27452 MW; 9087953BAFAVED25 CRC64;  
Query Match 49.4%; Score 621; DB 1; Length 251;  
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Matches 113; Conservative 37; Mismatches 74; Indels 6; Gaps 2;  
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DB 25 IIGHTCTRSSQPMQALLAAPPRLFCGALLGQWITAHGCRPLCYALKHNLR 84  
QY 59 EEGCQTRPATESPPHGFNNLSLNDKRDNDITLVKASPVSTIWAYRPLTLSSRCTAG 118  
DB 85 WEATQVAVRVRCVTHPVYN-----SRTHNDLMLLOQOPRIARAVPIEVTOACASPG 140  
QY 119 TSCLSGWSGTSPPQLRPHILRCANITIIHOKCENAYPGNDITWYCASVGGKQSC 178  
DB 141 TSCRVSAGTSSPFLARFASLQCNINISDEVCCQRAYPRTIIPGVCYCAVPGQKQSC 200  
QY 179 QGDSGGLVPCVQSLGQISWQDPCALTRKGYVTKYCKYVWIOETWN 228  
DB 201 QGDSGGLVPCVQSLGQISWQDPCALTRKGYVTKYCKYVWIOETWN 250  
RESULT 10  
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ID KLC6 HUMAN  
AC Q9URF0; Q9URF1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5) (KLC15).  
GN KLC12 OR KLC15.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4."  
RL Anticancer Res. 19:2843-2852 (1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Yousef G.M., Maglars A., Scoriilas A., Diamandis E.P.;  
RT "Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLC15)."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepker B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region."  
 RL Gene 257:119-130(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,  
 RA Danganan L., Ertler A., Christensen M., Georgescu A., Ayala J., Liu S.,  
 RA Dharre S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Truong S., Kobayashi A.,  
 RA Olsen A.S., Carraro A.V.;  
 RT "Sequence analysis of chromosome 19q13.4."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBS databases.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9UKR0-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
 CC -1- SIMILARITY: Belongs to peptidase family S1. kallikrein subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; ARI35025; AAD26426.2; -;  
 DR EMBL; ARI35025; AAF06065.1; -;  
 DR EMBL; AF243527; AAG3365.1; -;  
 DR EMBL; AC011473; AAG32558.1; -;  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.020; -;  
 DR Genew; HGNC:6360; KLU12.  
 DR MIM; 605539; -;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0004552; F:serine-type endopeptidase activity; NAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYPsin DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KW Hydroxylase, serine protease, Glycoprotein, Signal;  
 KW Alternative splicing.  
 FT CHAIN 1 17 POTENTIAL.  
 FT ACT\_SITE 18 248 KALLIKREIN 12.  
 FT ACT\_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 28 161 BY SIMILARITY.  
 FT DISULFID 47 63 BY SIMILARITY.  
 FT DISULFID 133 235 BY SIMILARITY.  
 FT DISULFID 140 206 BY SIMILARITY.  
 FT DISULFID 172 186 BY SIMILARITY.  
 FT DISULFID 195 222 BY SIMILARITY.  
 FT CARBOHYD 24 224 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 236 248 KYDWMRTMTRNN -> NSTLVGLGTSNMNFCQCP (in

FT isoform 2).  
 FT /FTId=VSP\_005403; CRC64;  
 SQ SEQUENCE 248 AA; 26733 MW; BB47398F8BAF703 Best Local Similarity 49.6%; Score 606; DB 1; Length 248;  
 Query Match 49.6%; Pred. No. 7,7e-49;  
 Matches 114; Conservative 33; Mismatches 79; Indels 4; Gaps 3;  
 QY 1 IIKGPECKPHSQPQOALLFETKRLLCATLIPAWMLTAHACLKPRITVHLGCHNLOKE 60  
 DB 22 IFNTEGGRNSQPPQVGLFBGTSLRCGVGLIDHWVLTAAHCGSRWVLGHSLSQLD 81  
 QY 61 GCEQTPRATESFPFPGGNNSLPNKDRNDMLVMASPVSIITVAVRPLTSSRCVYAGTS 120  
 DB 82 WTEQIRHSGFVTHPTGLGA--STSHEDLRRLRLRPVAVTSSVQPLPLPNCATATGE 139  
 QY 121 CLISGKSTSPQRLPHTLRCAANTTIEOKCEMAYPNITDTMVCAVQEGKDSQCG 160  
 DB 140 CHVGSGWGTTHFRNPFBDLLQCLNLISVSHATCGVYGRITSNMCAAG-GVPGDACAQ 198  
 QY 181 DSGGPLYVGNLSLGIISMGQ-DPCAIRKPGVYTKVCKYDWTQETMKN 229  
 DB 199 DSGGPLYVGGVGLQGLVMSGVGPGDGIPEVITTYICKYDWMTRMTRNN 248  
 RESULT 11  
 KLU1 RAT STANDARD; PRT; 261 AA.  
 AC P00758;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue  
 DE kallikrein) (PS kallikrein) (RGK-1).  
 GN KLU1 OR KLU-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83117659; PubMed=6961406;  
 RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;  
 RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid  
 RT sequence of the encoded preproenzyme."  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Submaxillary gland;  
 RX MEDLINE=86051477; PubMed=2998455;  
 RA Ashley P.L., MacDonald R.J.;  
 RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide  
 RT sequences of four distinct types including tonin."  
 RL Biochemistry 24:4512-4520(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=89327211; PubMed=2753879;  
 RA Inoue H., Fukui K., Miyake Y.;  
 RT "Identification and structure of the rat true tissue kallikrein gene  
 RT expressed in the kidney."  
 RL J. Biochem. 105:834-840(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89214217; PubMed=2708383;  
 RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., MacDonald R.J.;  
 RT "Organization and expression of the rat kallikrein gene family."  
 RL J. Biol. Chem. 264:7653-7662(1989).  
 RN [5]  
 RP SEQUENCE OF 48-261 PRO N.A.  
 RX MEDLINE=86131678; PubMed=3004582;  
 RA Gerald W.U., Chao J., Chao L.;  
 RT "Immunological identification of rat tissue kallikrein cDNA and

RT Characterization of the kallikrein gene family.";  
 RL Biochim. Biophys. Acta 866:1-14(1986).  
 CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds  
 CC in kininogen to release Lys-bradykinin.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J00758; -; NOT ANNOTATED CDS.  
 DR EMBL: M11563; AAA41464.1; ALT\_INIT.  
 DR EMBL: M23876; AAA41462.1; -.  
 DR EMBL: M23874; AAA41462.1; JOINED.  
 DR EMBL: M23875; AAA41462.1; JOINED.  
 DR EMBL: D00448; BAA00346.1; ALT\_INIT.  
 DR EMBL: D00446; BAA00346.1; JOINED.  
 DR EMBL: D00447; BAA00346.1; JOINED.  
 DR EMBL: X03560; CAA27247.1; -.  
 DR PIR: A00944; KORTP.  
 DR HSSP: P00757; ISGF.  
 DR MEROPS: S01.405; -.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; serine protease; Glycoprotein; Multigene family; Zymogen;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24 PROBABLE.  
 FT CHAIN 25 261 ACTIVATION PEPTIDE (PROBABLE).  
 FT CHAIN 1 111 GLANDULAR KALLIKREIN 1.  
 FT CHAIN 2 261  
 FT ACT\_SITE 65 65 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 213 213 CHARGE RELAY SYSTEM.  
 FT DISULFID 31 173 BY SIMILARITY.  
 FT DISULFID 50 66 BY SIMILARITY.  
 FT DISULFID 152 219 BY SIMILARITY.  
 FT DISULFID 184 198 BY SIMILARITY.  
 FT DISULFID 209 234 BY SIMILARITY.  
 FT CARBOHYD 108 108 N-LINKED (GLCNAC... ) (PROBABLE).  
 SQ SEQUENCE 261 AA; 28852 MW; F2F99C0227A7882B CRC64;  
 Query Match 48.1%; Score 605.5; DB 1; Length 261;  
 Best Local Similarity 45.1%; Pred. No. 9, 1e-49;  
 Matches 107; Conservative 43; Mismatches 79; Indels 7; Gaps 1;

QY 174 GKDSGQSGSGPPLVNCNSLGGIISWGDDPCALTRKPGVYTKCKYVDIMQETKKN 229  
 DB 205 GKDTCKSGSGGPIPLCNVGLGITSWGFNPGCEPKPGIYTLIRFTPEIKEMKEN 260  
 RESULT 12  
 ID KAT7\_RAT STANDARD; PRT; 261 AA.  
 AC P36373;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last annotation update)  
 DE Glandular kallikrein 7, submandibular/renal precursor (EC 3.4.21.35)  
 DE (Tissue kallikrein) (RKG-7) (RSKG-7) (Esterase B) (Proteinase A).  
 GN KUK7 OR KUK-7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCB:Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89086074; Pubmed=2849988;  
 RA Chen Y.-P., Chao J., Chao L.;  
 RT "Molecular cloning and characterization of two rat renal kallikrein  
 genes";  
 RL Biochemistry 27:7189-7196(1988).  
 RN [2]  
 RP SEQUENCE OF 25-75.  
 RC TISSUE=Submaxillary gland;  
 RX MEDLINE=88198057; Pubmed=3482210;  
 RA Kato H., Nakashishi E., Enjoji K., Hayashi I., Oh-Ishi S., Iwanaga S.;  
 RT "Characterization of serine proteinases isolated from rat  
 RT submaxillary gland: with special reference to the degradation of rat  
 RT kininogens by these enzymes";  
 RL J. Biochem. 102:1389-1404(1987).  
 CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds  
 CC in kininogen to release Lys-bradykinin.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- TISSUE SPECIFICITY: Kidney and submandibular gland.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
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 CC -----  
 DR EMBL: M19647; AAA41461.1; -.  
 DR PIR: A31136; A31136.  
 DR HSSP: P00759; ITON.  
 DR MEROPS: S01.406; -.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; serine protease; Glycoprotein; Multigene family; Zymogen;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24 PROBABLE.  
 FT CHAIN 25 261 GLANDULAR KALLIKREIN 7,  
 FT CHAIN 1 111 SUBMANDIBULAR/RENAL.  
 FT ACT\_SITE 65 65 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 120 120 CHARGE RELAY SYSTEM.

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FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 35 35 S -> D (IN REF. 2).
FT CONFLICT 46 46 T -> S (IN REF. 2).
SQ SEQUENCE 261 AA; 28972 MW; 4PB06C422F25A616 CRC64;

Query March 47.7%; Score 600.5; DB 1; Length 261;
Best Local Similarity 46.2%; Pred. No. 2.6e-48;
Matches 109; Conservative 39; Mismatches 81; Indels 7; Gaps 1;

QY 1 IIKGFECKPHSOPWQALFEKRLTLCATLLAPRMLTAACTAPRYVHLGQNLQXEE 60
   114 CVAAGTSCISGWSGTSSTPQLRPHLRCAITITIHOKCENAYPNITDWCASVQEG 173
   145 EPRVGSCTLASGWSGTPLWEPDDQCYNHLLNEKICIKYKEXVTDMLCAGLEEG 204
   174 GKDCSCGDSGSPVNCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 229
   205 GKDTCTGDSGSPVLCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 260

DB 85 PFAOHRVSSQSPFHPDVKRPFIMNHRKPPDDHSDMLHLHSQPADITDGVKVDLPTE 144
   114 CVAAGTSCISGWSGTSSTPQLRPHLRCAITITIHOKCENAYPNITDWCASVQEG 173
   145 EPRVGSCTLASGWSGTPLWEPDDQCYNHLLNEKICIKYKEXVTDMLCAGLEEG 204
   174 GKDCSCGDSGSPVNCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 229
   205 GKDTCTGDSGSPVLCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 260

QY 174 GKDCSCGDSGSPVNCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 229
   205 GKDTCTGDSGSPVLCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 260

DB 205 GKDTCTGDSGSPVLCQSLGIIISWQDPCATIRKFGVYTKVYDWTQETMKN 260

RESULT 13
ID KUK3_MOUSE STANDARD; PRT; 261 AA.
AC P00756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
DE (MGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
GN KUK3 OR KUK-3 OR NGFG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=85076169; Pubmed=6548955;
RA Ullrich A., Gray A., Wood W.L., Hayflick J., Seeburg P.H.;
RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
RT nerve growth factor using a high-stringency selection procedure.";
RL DNA 3:387-392(1984).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=85257431; Pubmed=3848399;
RA Evans B.A., Richards R.I.;
RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
RT are contiguous.";
RL EMBL J. 4:133-138(1985).
RN 13
RP SEQUENCE OF 25-261.
RX MEDLINE=81264363; Pubmed=7263706;
RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
RT gland 7 S nerve growth factor.";
RL J. Biol. Chem. 256:9156-9166(1981).
RN 14
RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
RC STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
RX MEDLINE=98035451; Pubmed=9351801;
RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.Q.;
RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
```

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RT four binding proteins.";
RL Structure 5:1275-1285(1997).
CC -1- FUNCTION: 7S NGF alpha chain stabilizes the 7S complex. The beta
CC dimer promotes neurite growth. The gamma chain is an arginine-
CC specific protease; it may also have plasminogen activator
CC activity as well as mitogenic activity for chick embryo
CC fibroblasts.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallikrein (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-Xaa or Leu-Xaa.
CC -1- COFACTOR: Binds 2 zinc ions per 7S complex. The zinc ions are
CC bound at the alpha-gamma interfaces.
CC -1- SUBUNIT: 7S nerve growth factor is composed of two alpha chains,
CC a beta dimer composed of identical chains, and two gamma chains.
CC -1- MISCELLANEOUS: This precursor is cleaved into segments to produce
CC the active form of the gamma chain, which occurs naturally as
CC combinations of either two or three segments held together by
CC disulfide bonds: B1 and A, or B1, C and B2.
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC -----
DR EMBL; X01389; CAA25645.1; -
DR EMBL; X01798; CAA25928.1; -
DR EMBL; X01799; CAA25930.1; -
DR PIR; A91005; NCMNG.
DR PDB; 1SGF; 27-MAY-98.
DR MEROPS; S01.170; -.
DR MGJ; WGI; 97322; NGFg.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KX Hydroxylase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Metal-Binding; Zinc; Signal; Growth factor; 3D-structure.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 261
FT CHAIN 25 107
FT CHAIN 112 261
FT ACT_SITE 65 65
FT ACT_SITE 120 120
FT ACT_SITE 213 213
FT ACT_SITE 231 231
FT METAL 236 236
FT METAL 236 236
FT DISULFID 31 173
FT DISULFID 50 66
FT DISULFID 152 219
FT DISULFID 184 198
FT DISULFID 209 234
FT CARBOHYD 102 102
FT CARBOHYD 102 107
FT DOVAIN 25 107
FT DOVAIN 112 261
FT DOVAIN 112 261
FT DOVAIN 165 261
FT CONFLICT 108 111
FT STRAND 26 26
FT STRAND 29 30
FT STRAND 33 35
FT HELIX 37 38
FT TURN 39 44
FT STRAND 44 44
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FT TURN 45 46  
 FT STRAND 47 56  
 FT TURN 57 58  
 FT STRAND 59 62  
 FT HELIX 64 66  
 FT STRAND 72 75  
 FT STRAND 79 79  
 FT TURN 80 81  
 FT TURN 85 86  
 FT STRAND 88 97  
 FT TURN 99 100  
 FT HELIX 103 105  
 FT TURN 118 119  
 FT STRAND 122 126  
 FT TURN 148 149  
 FT STRAND 151 156  
 FT STRAND 159 159  
 FT STRAND 167 167  
 FT STRAND 170 170  
 FT STRAND 172 179  
 FT HELIX 181 187  
 FT TURN 194 195  
 FT STRAND 196 200  
 FT STRAND 207 207  
 FT TURN 210 211  
 FT TURN 213 214  
 FT STRAND 216 219  
 FT TURN 220 221  
 FT STRAND 222 229  
 FT TURN 234 235  
 FT TURN 237 238  
 FT STRAND 241 245  
 FT HELIX 246 249  
 FT HELIX 250 258  
 FT TURN 259 259  
 SQ SEQUENCE 261 AA; 28998 MW; 4870748B174AF7C8 CRC64;

Query Match 47.3%; Score 595.5; DB 1; Length 261;  
 Best Local Similarity 44.5%; Pred. No. 7.6e-48;  
 Matches 105; Conservative 46; Mismatches 78; Indels 7; Gaps 1;

QY 1 IIKGFECKPHSQWQALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHLGQHNLOKEE 60  
 DB 25 IVGGFCEKNSQWVAVRYTOYLOGVLLDPNWLTAHCYDDNYKVLGKNNLFKDE 84  
 QY 61 GCEQTRATESFPHGPNNSLPNK-----DHRNDIMLVKQASPVSTWAVRPLTSSR 113  
 DB 85 PSAQHFVSKAIPHPGFNMSIMRKHIRELYDYSNDMLRLSKPADITDVKETLPTPE 144  
 QY 114 CVTAGTSCILSGWGTSSPOLRLPHLTRCANITIIHOCENAVPNTIDTMVCAVQSG 173  
 DB 145 EPRVLSGTCLASGWSITPTPEFTDLYCNLKLNEOCARHAEKVTDAMLCAEMDMG 204  
 QY 174 GKSDCCGDSGSPVYCNQSLQGLISWQODPCATRKSGVYTKVCKYVDMIOETMKNN 229  
 DB 205 KMDTKGDSGGPILCGVIGITISWGHTPCGERDMGVTTKMKFMSWKDMAXN 260

RESULT 14  
 ID TRY3 CHICK STANDARD; PRT; 248 AA.  
 AC Q90629;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Trypsin II-P29 precursor (EC 3.4.21.4).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas; PubMed=7733885;  
 RA MEDLINE=95251611; Hood L.E.;  
 RT "Isolation and characterization of the chicken trypsinogen gene family.";  
 RL Biochem. J. 307:471-479(1995).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Xaa, Lys-Xaa.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL: U15157; AAA79914.1; -;  
 DR PIR: S55066; S55066.  
 DR HSR: F00763; IDPO.  
 DR MEROPS: S01.151; -;  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYD\_SPC; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase: Serine protease; Digestion; Pancreas; Zymogen;  
 KM Calcium-binding; Signal; Multigene family.  
 FT SIGNAL 1 16  
 FT PROPEP 17 25  
 FT CHAIN 26 248  
 FT ACT\_SITE 65 65  
 FT METAL 77 77  
 FT METAL 79 79  
 FT METAL 82 82  
 FT METAL 87 87  
 FT ACT\_SITE 109 109  
 FT ACT\_SITE 202 202  
 FT DISULFID 32 162  
 FT DISULFID 50 66  
 FT DISULFID 134 235  
 FT DISULFID 141 208  
 FT DISULFID 173 187  
 FT DISULFID 198 222  
 FT SITE 196 196  
 SQ SEQUENCE 248 AA; 26622 MW; E5E16B0762258858 CRC64;

Query Match 47.2%; Score 594; DB 1; Length 248;  
 Best Local Similarity 49.6%; Pred. No. 9.9e-48;  
 Matches 112; Conservative 35; Mismatches 73; Indels 6; Gaps 3;

QY 1 IIKGFECKPHSQWQALFEKTRLLCGATLIPRMLTAAHCLKPRYIVHLGQHNLOKEE 60  
 DB 26 IVGGTCEHSEVYQVSL-NSGHPFCGSLNSGWSVAACVYSRQVRAEYNIDVGE 84  
 QY 61 GCEQTRATESFPHGPNNSLPNDHRNDIMLVKQASPVSTWAVRPLTSSRCVYTGTS 120  
 DB 85 DSEVRSSTSVIRHPKYSITLN-----NDIMLVKQASPVSTWAVRPLTSSRCVYTGTS 140  
 QY 121 CLISGWSGTSSPOLRLPHLTRCANITIIHOCENAVPNTIDTMVCAVQSGKDSGCG 180  
 DB 141 CLISGWSGTSSPOLRLPHLTRCANITIIHOCENAVPNTIDTMVCAVQSGKDSGCG 200

QY 181 DSGPVLVNCNLSGQITISWGDPICATIRKPGVYTKVCKYVDMIOETM 226  
 DB 201 DSGPVLVNCNLSGQITISWGIG-CALXGPGVYTKVCKYVDMIOETI 245

## RESULT 15

KLXK\_PRANA STANDARD; PRT; 263 AA.

AC P32824;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue kallikrein).  
 OS Prionyx natalensis (African soft-furred rat) (Mastomys natalensis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 OC Mastomys.  
 OX NCBI\_TaxID=10112;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary gland;  
 RX MEDLINE=94226702; PubMed=7909667;  
 RA Fahnestock M.;  
 RT "Characterization of kallikrein cDNAs from the African rodent Mastomys."  
 RL DNA Cell Biol. 13:293-300(1994).  
 CC -1- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release Lys-bradykinin.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg|-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of Met|-Xaa or Leu|-Xaa.  
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X17352; CA93232.1; --  
 DR PIR; I83227; S15686.  
 DR HSP; P00757; ISGF.  
 DR MEROPS; S01.160; --  
 DR InterPro: IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; serine protease; Glycoprotein; Multigene family; Zymogen; signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 24 PROBABLE.  
 FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.  
 FT ACT\_SITE 65 65 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 121 121 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 215 215 CHARGE RELAY SYSTEM.  
 FT DISULFID 31 175 BY SIMILARITY.  
 FT DISULFID 50 66 BY SIMILARITY.  
 FT DISULFID 153 221 BY SIMILARITY.  
 FT DISULFID 186 200 BY SIMILARITY.  
 FT DISULFID 211 236 BY SIMILARITY.  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC... ) (PROBABLE).  
 SQ SEQUENCE 263 AA; 29130 MM; A8EB023B80037D5 CRC64;

Query Match 47.0%; Score 591.5; DB 1; length 263;

Best Local Similarity 44.5%; Pred. No. 1.8e-47;  
 Matches 106; Conservative 44; Mismatches 79; Indels 9; Gaps 2;  
 QY 1 IIKGPECKPSQEPQOALLFEKTRLLCGATLIAPRMLITAHCLKPRITVHLSGNLQKE 60  
 DB 25 IIGFNECKNSQPMHVAVYRFRARQCGVLLDANWVLTAAHCNDKIQVWLGNNRFEDE 84  
 QY 61 GCEOTRATESFPFGFNNSLPNKDH-----RNDIMLVKASPVYSITWAVRPLTSS 112  
 DB 85 PSAQHOLSKAIPHPGFMSLINKDHPHEBDYXNDMLVRLKKPAETIDVYKPIDLPT 144  
 QY 113 RCVTAGTISCLISNGSTS-SPQLRPLTLPCANITIEHOKCENAPGNITDMVCAVQ 171  
 DB 145 EEPVVGSRCLASGWSITPTEFEFYSHDLCVLELISNEVCAKAKTEKVTDTMLCGEM 204  
 QY 172 EGGKDSGCGSPVLVNCNLSGQITISWGDPICATIRKPGVYTKVCKYVDMIOETMKN 229  
 DB 205 DSGKDTVGDGSGPLICDGVLOGITISWGPFCALPNVPGIYTLIEYRSIKVWMANN 262

Search completed: June 22, 2004, 18:55:21  
 Job time : 18 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 22, 2004, 18:53:42 ; Search time 22 Seconds

(without alignments)  
537.379 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIKGFCECKPHSQPWQALFE.....GVYTKCKYVDIQTWKNN 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep: \*  
6: /cgn2\_6/ptodata/2/1aa/6D.COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	US-09-205-258-427	Sequence 427, App
2	1258	100.0	282	US-09-025-059-1	Sequence 1, Appl
3	1227	97.5	248	US-08-944-483-24	Sequence 24, Appl
4	1219.5	96.9	289	US-09-386-642-14	Sequence 14, Appl
5	684	54.4	260	US-09-025-059-3	Sequence 3, Appl
6	684	54.4	260	US-09-618-259-8	Sequence 8, Appl
7	681	54.1	260	US-09-070-526-2	Sequence 2, Appl
8	681	54.1	260	US-09-618-259-7	Sequence 7, Appl
9	673	53.5	260	US-09-008-271A-7	Sequence 7, Appl
10	671.5	53.4	288	US-09-386-642-13	Sequence 13, Appl
11	651	51.7	228	US-09-205-258-1150	Sequence 1150, Ap
12	651	51.7	246	US-09-205-258-1149	Sequence 1149, Ap
13	644.5	51.2	293	US-09-509-908-2	Sequence 2, Appl
14	597.5	47.5	268	US-08-824-874-1	Sequence 1, Appl
15	597.5	47.5	268	US-09-210-084-1	Sequence 1, Appl
16	597.5	47.5	268	US-09-764-762-1	Sequence 1, Appl
17	591.5	47.0	263	US-08-790-137-4	Sequence 4, Appl
18	591.5	47.0	263	US-08-824-874-5	Sequence 5, Appl
19	591.5	47.0	263	US-08-802-151-5	Sequence 5, Appl
20	591.5	47.0	263	US-09-210-084-5	Sequence 5, Appl
21	591.5	47.0	263	US-08-478-957-5	Sequence 5, Appl
22	591.5	47.0	263	US-09-764-762-5	Sequence 5, Appl
23	587	46.7	246	US-08-978-404B-44	Sequence 44, Appl
24	577.5	45.9	232	US-08-978-404B-45	Sequence 45, Appl
25	577.5	45.9	232	US-08-768-859A-16	Sequence 16, Appl
26	577.5	45.9	237	US-08-767-820A-15	Sequence 15, Appl
27	577.5	45.9	237	US-08-622-046B-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-09-205-258-427  
Sequence 427, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06

28	577.5	45.9	237	3	US-08-944-483-37	Sequence 37, Appl
29	577.5	45.9	237	3	US-09-100-264-1	Sequence 1, Appl
30	577.5	45.9	237	4	US-08-843-076D-1	Sequence 1, Appl
31	577.5	45.9	238	3	US-08-768-859A-8	Sequence 8, Appl
32	577.5	45.9	238	3	US-08-767-820A-8	Sequence 8, Appl
33	577.5	45.9	244	3	US-08-768-859A-10	Sequence 10, Appl
34	577.5	45.9	244	3	US-08-767-820A-10	Sequence 10, Appl
35	577.5	45.9	244	3	US-08-622-046B-16	Sequence 16, Appl
36	577.5	45.9	244	3	US-09-100-264-5	Sequence 5, Appl
37	577.5	45.9	244	4	US-08-843-076D-5	Sequence 5, Appl
38	577.5	45.9	261	3	US-08-768-859A-6	Sequence 6, Appl
39	577.5	45.9	261	3	US-08-622-046B-14	Sequence 6, Appl
40	577.5	45.9	261	3	US-09-100-264-7	Sequence 7, Appl
41	577.5	45.9	261	4	US-08-983-075D-7	Sequence 7, Appl
42	577.5	45.9	261	4	US-08-843-076D-3	Sequence 3, Appl
43	577.5	45.9	228	1	US-08-278-091-7	Sequence 7, Appl
44	577	45.9	228	1	US-08-483-859-7	Sequence 7, Appl
45	577	45.9	228	1	US-08-483-859-7	Sequence 7, Appl

EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO: 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-427

Query Match 100.0%; Score 1258; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.5e-125;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSOPMOALFEKTRLLCGATLLAPRWLLTAACHLKRYIVHGGHNLQKEE 60  
DB 22 IIKGFECKPHSOPMOALFEKTRLLCGATLLAPRWLLTAACHLKRYIVHGGHNLQKEE 81  
QY 61 GCEQRTATESFPHGFNNSLPNKDRNDIMLVKASPVSTIWAVRPLTLSSRCVYAGTS 120  
DB 82 GCEQRTATESFPHGFNNSLPNKDRNDIMLVKASPVSTIWAVRPLTLSSRCVYAGTS 141  
QY 121 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYNGNITDTMVCASVDEGGKDSGCG 180  
DB 142 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYNGNITDTMVCASVDEGGKDSGCG 201  
QY 181 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVCKYVDVIOETMKN 229  
DB 202 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVCKYVDVIOETMKN 250

RESULT 2  
US-09-025-059-1  
Sequence 1, Application US/09025059  
Patent No. 6075136

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGUT110  
CLONE: 2723646  
US-09-025-059-1

Query Match 100.0%; Score 1258; DB 3; Length 282;  
Best Local Similarity 100.0%; Pred. No. 1.8e-125;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSOPMOALFEKTRLLCGATLLAPRWLLTAACHLKRYIVHGGHNLQKEE 60  
DB 54 IIKGFECKPHSOPMOALFEKTRLLCGATLLAPRWLLTAACHLKRYIVHGGHNLQKEE 113  
QY 61 GCEQRTATESFPHGFNNSLPNKDRNDIMLVKASPVSTIWAVRPLTLSSRCVYAGTS 120  
DB 114 GCEQRTATESFPHGFNNSLPNKDRNDIMLVKASPVSTIWAVRPLTLSSRCVYAGTS 173  
QY 121 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYNGNITDTMVCASVDEGGKDSGCG 180  
DB 174 CLISWGSTSSPOLRLPHTLRCAITIIIEHOKCENAYNGNITDTMVCASVDEGGKDSGCG 233  
QY 234 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVCKYVDVIOETMKN 282  
DB 282 DSGGPLVNCOSLOGIISWGDPICATTRKPGVYTKVCKYVDVIOETMKN 329

RESULT 3  
US-08-944-483-24  
Sequence 24, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COPIETS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.

APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
TITLE OF INVENTION: OF THE PROSTATE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183. US. 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6232456e  
US-08-944-483-24

Query Match 97.5%; Score 1227; DB 3; Length 248;  
Best Local Similarity 99.1%; Pred. No. 3e-122;  
Matches 227; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 IIKGFEC-KPHSQWQALFEKTRLLCGATLIAPRWLLTAACHCKPRYIVHVGHNLOKE 60  
DB 22 IIKGFEC-PHSQWQALF-KTRLLCGATLIAPRWLLTAACHCKPRYIVHVGHNLOKE 79

QY 61 GCEQTRATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 120  
DB 80 GCEQTRATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 139

QY 121 CLISGWSSTSPQRLPHTLRCAITIIHOKCENAPGNITDTMVCASVOEGKDSQ 180  
DB 140 CLISGWSSTSPQRLPHTLRCAITIIHOKCENAPGNITDTMVCASVOEGKDSQ 199

QY 181 DSGGPLVNCNLSGIIISWGDPCAITRKPGVYTKCKYVDWIQETMKN 229  
DB 200 DSGGPLVNCNLSGIIISWGDPCAITRKPGVYTKCKYVDWIQETMKN 248

RESULT 4  
US-09-386-642-14  
Sequence 14, Application US/09386642  
Patent No. 6420157  
GENERAL INFORMATION:  
APPLICANT: Darrow, Andrew  
APPLICANT: Qi, Jensen

APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386,642  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 289  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14

Query Match 96.9%; Score 1219.5; DB 4; Length 289;  
Best Local Similarity 97.0%; Pred. No. 2.3e-121;  
Matches 223; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 IIKGFEC-KPHSQWQALFEKTRLLCGATLIAPRWLLTAACHCKPRYIVHVGHNLOKE 59  
DB 52 IYGVNCLSKHSQPWQALFEKTRLLCGATLIAPRWLLTAACHCKPRYIVHVGHNLOKE 111

QY 60 ECEQTRATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 119  
DB 112 ECEQTRATSPFPHGFNNSLPNKDHNDIMLVKMASPVSIITAVRPLTLSSRCVTAGT 171

QY 120 SCLISGWSSTSPQRLPHTLRCAITIIHOKCENAPGNITDTMVCASVOEGKDSQ 179  
DB 172 SCLISGWSSTSPQRLPHTLRCAITIIHOKCENAPGNITDTMVCASVOEGKDSQ 231

QY 180 DSGGPLVNCNLSGIIISWGDPCAITRKPGVYTKCKYVDWIQETMKN 229  
DB 232 DSGGPLVNCNLSGIIISWGDPCAITRKPGVYTKCKYVDWIQETMKN 281

RESULT 5  
US-09-025-059-3  
Sequence 3, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guesler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1020091  
US-09-025-059-3

Query Match 54.4%; Score 684; DB 3; Length 260;  
Best Local Similarity 53.1%; Pred. No. 1.5e-64;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWQALFEKTRLLCGATLIAAPWLLTAHCLKPRYIVHLGQHNLOKEE 60  
DB 33 ILERECIPHSQWQWQALFQGERLICGVALVGDWVLTAAHCKKQKSVRLGDSHQSD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVPLTSSRCVTAGTS 120  
DB 93 QPEGEIQAOSIQHPCCYNNSP-EDSHDMLIRLQNSANLGDKXRVOLANICPRVQOK 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTWVCASVQEGKDCSCG 180  
DB 152 CLISGWSGTVTSPQENPNTLNCALVKIYSQKCEBAPFGKITEGWVCAQ-SSNGADTCQG 210  
QY 181 DSGGPLVNCOSLOGIISWGDPQCAITRPGVYTKVCKYVDMIOETMKN 228  
DB 211 DSGGPLVCDGMLQGITSMGSDPCGKPKPGVYTKICRYTTWIKTKMDN 258

RESULT 6  
US-09-618-259-8  
Sequence 8, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
FILE REFERENCE: D6020CIP2  
CURRENT APPLICATION NUMBER: US/09/618, 259  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: US 09/127,444  
PRIOR FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 8  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURES:  
OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous  
OTHER INFORMATION: to TMDG-14; accession no. D30785  
US-09-618-259-8

Query Match 54.4%; Score 684; DB 4; Length 260;  
Best Local Similarity 53.1%; Pred. No. 1.5e-64;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWQALFEKTRLLCGATLIAAPWLLTAHCLKPRYIVHLGQHNLOKEE 60  
DB 33 ILERECIPHSQWQWQALFQGERLICGVALVGDWVLTAAHCKKQKSVRLGDSHQSD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVPLTSSRCVTAGTS 120  
DB 93 QPEGEIQAOSIQHPCCYNNSP-EDSHDMLIRLQNSANLGDKXRVOLANICPRVQOK 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTWVCASVQEGKDCSCG 180  
DB 152 CLISGWSGTVTSPQENPNTLNCALVKIYSQKCEBAPFGKITEGWVCAQ-SSNGADTCQG 210  
QY 181 DSGGPLVNCOSLOGIISWGDPQCAITRPGVYTKVCKYVDMIOETMKN 228

DB 211 DSGGPLVCDGMLQGITSMGSDPCGKPKPGVYTKICRYTTWIKTKMDN 258

RESULT 7  
US-09-070-526-2  
Sequence 2, Application US/09070526  
Patent No. 610059  
GENERAL INFORMATION:  
APPLICANT: SOUTHAN, CHRISTOPHER  
APPLICANT: CLINKENBEARD, HELEN  
APPLICANT: BURGESS, NICOLA  
TITLE OF INVENTION: No. 6100059el Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATTNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070, 526  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9711952.3  
FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-526-2

Query Match 54.1%; Score 681; DB 3; Length 260;  
Best Local Similarity 51.8%; Pred. No. 3e-64;  
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGFECKPHSQPQWQALFEKTRLLCGATLIAAPWLLTAHCLKPRYIVHLGQHNLOKEE 60  
DB 33 VLGHECCPHSQPQWQALFQGOQLCGVALVGNWVLTAAHCKKPKYTVRLGDSLONKD 92  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVPLTSSRCVTAGTS 120  
DB 93 GPEQEIPIVQOSIQHPCCYNNSS-DVEDNHNDMLQLRQASIGSKVKRISLADHTQGGOK 151  
QY 121 CLISGWSSTSPQRLPHTLRCAANTTIEHOKCENAPGNITPTWVCASVQEGKDCSCG 180  
DB 152 CLVSGMGTVTSPRENFPTLNCACAVKIFPQKCEBAPFGQITTDWVCASSKGA-DTCQG 210  
QY 181 DSGGPLVNCOSLOGIISWGDPQCAITRPGVYTKVCKYVDMIOE 224  
DB 211 DSGGPLVCDGMLQGITSMGSDPCGKPKPGVYTKICRYTTWIKTKMDN 254

## RESULT 8

US-09-618-259-7  
Sequence 7, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
APPLICANT: Underwood, Lowell J.  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
FILE REFERENCE: D6020CIP2  
CURRENT APPLICATION NUMBER: US/09/618,259  
PRIORITY FILING DATE: 2000-07-18  
PRIORITY FILING DATE: US 09/127,444  
PRIORITY FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 7  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of TADG-14 protein  
US-09-618-259-7

Query Match 54.1%; Score 681; DB 4; Length 260;  
Best Local Similarity 51.8%; Pred. No. 3e-64;  
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IIKGFECRPHSQPQALFEKTRILCGATLTAAPRMILTAHCKPRTYVHLGQHNLOKEE 60  
DB 33 VLGGEHCQPHSQPQALFQGGQLCGVLVGNWVLTAAHCKKPYTVLGDHSLQNKD 92  
QY 61 GCEQRTATSPFPHGNNSLPNKDRNDIMLVKMASPVSTIWAAYRPLTISRCTAGTS 120  
DB 93 GPEQELIPVQSIPIPCVNS-DVEDNHDMLQLQDQASLGSKVPISLADHCTQPGOK 151  
QY 121 CLISGWSSTSPQLRPLHTRCANITIEHQKCNAYPGNITDTWVCASVQEGGKDSQCG 180  
DB 152 CTVSGMGVTVSPRENFPDLTNCAYKIFPQKKCEDAYPGQITDGMVCAGSSKGA-DTCGG 210  
QY 181 DSGGPLVGNQSLGILISWGQDPCATIRKPGVYTKVKCYVDWIOE 224  
DB 211 DSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKK 254

## RESULT 9

US-09-008-271A-7  
Sequence 7, Application US/09008271A  
Patent No. 6203979  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Puryl  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998  
PRIORITY APPLICATION DATA:

## APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheila  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLNOT27  
CLONE: 1798496  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 53.5%; Score 673; DB 3; Length 260;  
Best Local Similarity 51.3%; Pred. No. 2.1e-63;  
Matches 115; Conservative 42; Mismatches 65; Indels 2; Gaps 2;

QY 1 IIKGFECRPHSQPQALFEKTRILCGATLTAAPRMILTAHCKPRTYVHLGQHNLOKEE 60  
DB 33 VLGGEHCQPHSQPQALFQGGQLCGVLVGNWVLTAAHCKKPYTVLGDHSLQNKD 92  
QY 61 GCEQRTATSPFPHGNNSLPNKDRNDIMLVKMASPVSTIWAAYRPLTISRCTAGTS 120  
DB 93 GPEQELIPVQSIPIPCVNS-DVEDNHDMLQLQDQASLGSKVPISLADHCTQPGOK 151  
QY 121 CLISGWSSTSPQLRPLHTRCANITIEHQKCNAYPGNITDTWVCASVQEGGKDSQCG 180  
DB 152 CTVSGMGVTVSPRENFPDLTNCAYKIFPQKKCEDAYPGQITDGMVCAGSSKGA-DTCGG 210  
QY 181 DSGGPLVGNQSLGILISWGQDPCATIRKPGVYTKVKCYVDWIOE 224  
DB 211 DSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKK 254

## RESULT 10

US-09-386-642-13  
Sequence 13, Application US/09386642  
Patent No. 6420157  
GENERAL INFORMATION:  
APPLICANT: Darlow, Andrew  
APPLICANT: Qi, Jensen  
APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386,642  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

Query Match 53.4%; Score 671.5; DB 4; Length 288;  
Best Local Similarity 51.6%; Pred. No. 3.6e-63;  
Matches 116; Conservative 42; Mismatches 64; Indels 3; Gaps 3;

QY 1 IIKGFECRPHSQPQALFEKTRILCGATLTAAPRMILTAHCKPRTYVHLGQHNLOKEE 59  
DB 52 IVGGINCLEPHSQPQALFQGGQLCGVLVGNWVLTAAHCKKPYTVLGDHSLQNK 111

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Qy 60 EGCQRTATSESPHGFENSLPNKHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 DGEFOEIPVVOQSIPIHPCYNSS-DVEDENHDMLOLRDQASLSGSKVPISLADHCTQPOQ 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 SCISWGSTSPOLRLPHLRCAANTTIEHOKCEANVPANITDTWVCAVSQEGKDSQ 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 KCTVSGVGTSPRENPDTLNCAEVKIFPKKCEDAYRQGITDGNVCASSGA-DTQ 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 180 GDSGGLVNCQSLQGITSWGDDPCATRKPGVYTKVYDWIOE 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 GDSGGLVNCQSLQGITSWGSDPCGRSDKPGVYTNICRYDWIMK 274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-205-258-1150
; Sequence 1150, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1150

Query Match 51.7%; Score 651; DB 4; length 228;
Best Local Similarity 91.7%; Pred. No. 3,9e-61;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 IIKGFECKPHSQPMQALFETRLLCGATLIAPRWMLTAHCLKPRITVHLGQNLQKEE 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 IIKGFECKHSPQPMQALFETRLLCGATLIAPRWMLTAHCLKPRITVHLGQNLQKEE 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 GCEQRTATSESPHGFENSLPNKHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 GCEQRTATSESPHGFENSLPNKHNDIMLVKASPVSTWAVRPLTSSRCVTAGT 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 121 CLISWGSTSP 132
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 CSFPAGARPDF 135
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-205-258-1149
; Sequence 1149, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
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Thu Jun 24 10:06:30 2004

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Page 7

EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
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EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
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EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1149  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-258-1149  
Query Match  
Best Local Similarity 51.7%; Score 651; DB 4; Length 246;  
Best Local Similarity 91.7%; Pred. No. 4.3e-61;  
Matches 121, Conservative 1, Mismatches 10, Indels 0, Gaps 0;  
QY 1 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRRIYVHGQNLQKEE 60  
DB 22 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRRIYVHGQNLQKEE 81  
QY 61 GGEQRTATSESPHGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GGEQRTATSESPHGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSSTSP 132  
DB 142 CSFPAARPD 153  
RESULT 13  
US-09-509-908-2  
; Sequence 2, Application US/09509908  
; Patent No. 6589770  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company, N/A N/A  
; TITLE OF INVENTION: A Protease  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: T. David Reed  
; STREET: 5299 Spring Grove Avenue  
; CITY: Cincinnati  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 45217-1097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/509,908  
; FILING DATE: 28-Feb-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, T. David  
; REGISTRATION NUMBER: 32,931  
; REFERENCE/DOCKET NUMBER: AA-264P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 513-627-7025  
; TELEFAX: 513-627-6333  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-509-908-2  
Query Match  
Best Local Similarity 51.2%; Score 644.5; DB 4; Length 293;  
Best Local Similarity 50.6%; Pred. No. 2.7e-60;  
Matches 117, Conservative 40, Mismatches 67, Indels 7, Gaps 4;  
QY 1 IIKGFCEKPHSQPQALFEKTRILCGATLLAPRWLLTAHCKRRIYVHGQNLQKEE 58  
DB 67 IINGSDCMHTQPMQADLLRPNGLYCGAVLVHPQMLLTAHCKRRIYVHGQNLQKEE 126  
QY 59 EBGCEQRTATSESPHGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAG 118

Db 127 YESQCMFGVKSI.FPHGYS---HFGHSDMLIKLNRRIRPTKQVRPINVSHSPSAG 182  
Qy 119 TSCLSGWSSTSPQLRPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKXSC 178  
Db 183 TKCLVSGMGTTSQVAFPKVLQCLINISVLQKRCEDAYPRQIDITMFCAG-DKAGRDSG 241  
Qy 179 QGDSGGLVNCOSLOGISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 242 QGDSGGLVNCOSLOGISWGDYPCARPNRGVYTNLCKFTKMIQETIQAN 292

## RESULT 14

US-08-824-874-1  
; Sequence 1, Application US/08824874  
; Patent No. 5862300  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; TITLE OF INVENTION: NOVEL KALLIKREIN  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/824,874  
; FILING DATE: Filed Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0252 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 268 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: KERANOTO2  
; CLONE: 820694  
US-08-824-874-1

Query Match 47.5%; Score 597.5; DB 2; Length 268;  
Best Local Similarity 49.1%; Pred. No. 2.3e-55;  
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4;  
Qy 7 CKPHSQPMQALFEKTRLLGATLIAPRWLLTAHCLKPRYIVHGOHNLQK-BEGGEOT 65  
Db 50 CTP-SRGAALLRPNDLYGCAVLVHPQMLTAHCKKRYRRLGHTISLSPYESSQGM 108  
Qy 66 RTATESPFPHPGNNLSLNKDRNDIMLVKMASPVSIWAVRPLTSSRCVYTAGTSLISG 125  
Db 109 FQGVKSI.FPHGYS---HFGHSDMLIKLNRRIRPTKQVRPINVSHSPSAGTKCLVSG 164  
Qy 126 WGSTSSPOLRLPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKXSCGDSGSGP 185  
Db 165 WGTYSPOVHPKVLQCLINISVLQKRCEDAYPRQIDITMFCAG-DKAGRDSGDSGSGP 223

Qy 186 LVNCOSLOGISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 224 VVNCOSLOGISWGDYPCARPNRGVYTNLCKFTKMIQETIQAN 267

## RESULT 15

US-09-210-084-1  
; Sequence 1, Application US/09210084  
; Patent No. 6197511  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; TITLE OF INVENTION: NOVEL KALLIKREIN  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/210,084  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/824,874  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0252 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 268 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: KERANOTO2  
; CLONE: 820694  
US-09-210-084-1

Query Match 47.5%; Score 597.5; DB 3; Length 268;  
Best Local Similarity 49.1%; Pred. No. 2.3e-55;  
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4;  
Qy 7 CKPHSQPMQALFEKTRLLGATLIAPRWLLTAHCLKPRYIVHGOHNLQK-BEGGEOT 65  
Db 50 CTP-SRGAALLRPNDLYGCAVLVHPQMLTAHCKKRYRRLGHTISLSPYESSQGM 108  
Qy 66 RTATESPFPHPGNNLSLNKDRNDIMLVKMASPVSIWAVRPLTSSRCVYTAGTSLISG 125  
Db 109 FQGVKSI.FPHGYS---HFGHSDMLIKLNRRIRPTKQVRPINVSHSPSAGTKCLVSG 164  
Qy 126 WGSTSSPOLRLPHLTRCANITIEHOKCENAYPGNITDTWVCASVQEGKXSCGDSGSGP 185  
Db 165 WGTYSPOVHPKVLQCLINISVLQKRCEDAYPRQIDITMFCAG-DKAGRDSGDSGSGP 223  
Qy 186 LVNCOSLOGISWGODPCATRRKPGVYTKVCKYVDWIOETMKN 229  
Db 224 VVNCOSLOGISWGDYPCARPNRGVYTNLCKFTKMIQETIQAN 267



Thu Jun 24 10:06:30 2004

us-09-856-320a-2\_copy\_54\_282.rai

Page 9

Search completed: June 22, 2004, 16:57:27  
Job time : 23 secs

***This Page Blank (uspio)***

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 22, 2004, 21:57:33 ; Search time 456 Seconds

(without alignments)  
2133.415 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIRGFCECKPHSGPWOALFE.....GVYTKYCKYVDIQTETKNN 229

Scoring table:

BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool\_p/US09856320/runat\_22062004\_172805\_11855/app\_query.fasta\_1.391  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	1106	2	AA222638
2	1258	100.0	1158	2	AA222639
3	1258	100.0	1186	6	ABK92131
4	1258	100.0	1186	7	ABX76468
5	1258	100.0	1186	9	ADB80595
6	1258	100.0	1186	9	ADB75387
7	1258	100.0	1192	4	AAD14842
8	1258	100.0	1204	3	AAA37072

9	1258	100.0	1204	4	AA554320	AA554320	DNA	encod
10	1258	100.0	1204	4	AA521496	AA521496	Human	CDN
11	1258	100.0	1204	6	ABK33628	ABK33628	CDNA	enco
12	1258	100.0	1204	6	ABL68175	ABL68175	Human	PRO
13	1258	100.0	1204	6	ABL95664	ABL95664	Human	ang
14	1258	100.0	1204	7	ACD24105	ACD24105	Human	hum
15	1258	100.0	1204	7	ACA66933	ACA66933	CDNA	enco
16	1258	100.0	1204	7	ACD68685	ACD68685	Novel	hum
17	1258	100.0	1204	7	ACA67246	ACA67246	CDNA	enco
18	1258	100.0	1204	7	ACA03855	ACA03855	CDNA	enco
19	1258	100.0	1204	7	ABX89393	ABX89393	DNA	enco
20	1258	100.0	1204	7	ACD42047	ACD42047	Human	sec
21	1258	100.0	1204	7	ACA68589	ACA68589	Novel	hum
22	1258	100.0	1204	7	ACA04276	ACA04276	Human	CDN
23	1258	100.0	1204	8	ADA46024	ADA46024	Novel	hum
24	1258	100.0	1204	8	ADA76455	ADA76455	Human	PRO
25	1258	100.0	1204	8	ABT44318	ABT44318	Human	PRO
26	1258	100.0	1204	8	ADA19105	ADA19105	Human	PRO
27	1258	100.0	1204	8	ADA61728	ADA61728	Human	PRO
28	1258	100.0	1204	8	ADB19513	ADB19513	Novel	sapi
29	1258	100.0	1204	8	ADB28054	ADB28054	CDNA	enco
30	1258	100.0	1204	8	ADA86533	ADA86533	Novel	hum
31	1258	100.0	1204	8	ADB16097	ADB16097	Human	PRO
32	1258	100.0	1204	8	ADA47883	ADA47883	Human	PRO
33	1258	100.0	1204	8	ACD68357	ACD68357	Novel	hum
34	1258	100.0	1204	8	ADA67678	ADA67678	Human	PRO
35	1258	100.0	1204	8	ADB30685	ADB30685	CDNA	enco
36	1258	100.0	1204	8	ADA85981	ADA85981	Novel	hum
37	1258	100.0	1204	8	ADA97193	ADA97193	Human	PRO
38	1258	100.0	1204	8	ADA79497	ADA79497	Human	PRO
39	1258	100.0	1204	8	ADA87636	ADA87636	Novel	hum
40	1258	100.0	1204	8	ADB16838	ADB16838	Human	PRO
41	1258	100.0	1204	8	ADA91930	ADA91930	Novel	hum
42	1258	100.0	1204	8	ADB14893	ADB14893	Human	hum
43	1258	100.0	1204	8	ADB18954	ADB18954	Novel	hum
44	1258	100.0	1204	8	ADA94169	ADA94169	Human	PRO
45	1258	100.0	1204	8	ADB20065	ADB20065	Novel	hum

## ALIGNMENTS

RESULT 1	AA222638	standard; cDNA; 1106 BP.
XX	ID	AA222638
XX	AC	AA222638;
XX	DT	08-DEC-1999 (first entry)
XX	DE	CASB12 nucleotide sequence.
XX	KW	neuropain; cancer; assay; inhibitor; serine protease; immunogenic; ds.
XX	OS	Homo sapiens.
XX	EH	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	14..862
XX	FT	/*tag= a
XX	FT	/product= "CASB12"
XX	PN	WO949055-A1.
XX	PD	30-SEP-1999.
XX	PP	17-MAR-1999; 99WO-EP001894.
XX	PR	20-MAR-1998; 98GB-00006095.
XX	PA	(SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX	PI	Bruck CEM, Cassart J, Coche T, Vinals-Bassols C,
DR	WPI	1999-580450/49.

DR P-PSDB; AAY42439.

XX PT New human serine protease CASB12, for treatment, prevention and diagnosis  
PT of cancer and autoimmune diseases.

XX Claim 10; Page 47; 58pp; English.

PS This is the nucleotide sequence of the CASB12 gene. The nucleotide  
CC sequence of AA222639 shows homology with neuropilin and the encoded  
CC protein AAY42439 is structurally related to other proteins of the serine  
CC protease family, having homology and/or structural similarity with  
CC neuropilin. It is expected that as well as similar structure, these  
CC proteins will also share similar biological functions and properties. The  
CC CASB12 polypeptides and polynucleotides can be used to develop methods  
CC for identifying agonists and antagonists/inhibitors of these molecules,  
CC and thereby treating conditions associated with CASB12 polypeptide  
CC imbalance. The invention also provides for diagnostic assays for  
CC detecting diseases associated with inappropriate CASB12 polypeptide  
CC activity or levels. Since CASB12 is either specifically expressed or  
CC highly over-expressed in tumors compared to normal cells, the  
CC polypeptides and polynucleotides of the invention are believed to be  
CC important immunogens for specific prophylactic or therapeutic  
CC immunization against tumors. The polypeptides and polynucleotides can  
CC therefore be targeted by antigen specific immune reactions (which result  
CC in the destruction of the tumor cell) or they can be used to diagnose the  
CC occurrence of tumor cells

XX Sequence 1106 BP; 247 A; 348 C; 287 G; 224 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 5,38e-104 Length: 1106  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x AA222638 (1-1106)

QY 1 IleIleIleYSGlyPheGluCyGlyPProHisSerGlnProTrpGlnAlaIleuPheGlu 20  
DB 173 ATCATCAAGGGGTTGAGTGCAGTCCATCCAGCCCTGGCGAGGAGCCCTGTGTGAG 232  
QY 21 LysThrArgLeuLeuCyGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40  
DB 233 AAGACGGCGTACTCTGTGGGCGACCGTCTATCCGCCAGATGGCTCCGACAGACGCC 292  
QY 41 HisCysLeuYsProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnYsGluGlu 60  
DB 293 CACTGCGCTCAAGCCCGCTCATAGTTCACCTGGGCGACGACCACTCCGAAAGAGAGAG 352  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 353 GGCTGTGAGCAGACCCGACAGCCACTGAGTCTCTCCGCCACCCCGCTTCMACACACAGC 412  
QY 81 LeuProAsnYsAspHisArgAsnAspIleuLeuValYsMetAlaSerProValSer 100  
DB 413 CTCCCAACAAAGACCAACCGCATGATCATGTGTGAAGATGAGCATGCCAGATCTCC 472  
QY 101 IleHrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 473 ATCACTGGGCTGTGCGACCCCTCACTCTCCACAGCTGTGTCATGCTGGACACAGC 532  
QY 121 CysLeuIleSerGlyTyrPGLySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 533 TGCCTCATTTCCGGCTGGGCGAGACGTCAGCCGCCAGTTAGCCCTGCTCACACCTTG 592  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnYsCysGluAsnAlaTyrProGlyAsn 160  
DB 593 CGATGCGCCAAATCATCATTCATGACACCAAGAGTGTAGAAAGCGCTCCCGGAC 652  
QY 161 IleHrAspTrpMetValCysAlaSerValGlnGlnGlyGlyYsAspSerCysGlnGly 180

DB 653 ATCAGACAGACCAATGCTGTGTGCCAGCTGACGAGAAAGGGCGAAGACTCTGTCAGAGGT 712  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
DB 713 GACTCGGGGGGCCCTGTGCTGTGTACACAGCTCTTCAGGCAATTCCTCTGGGGCCAG 772  
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220  
DB 773 GATTCGTGTGAGTATCCCGAAGCTGTGTCTACAGAAAGTGTGAAATATGTGGAC 832  
QY 221 TPILieGlnGlnThrMetLysAsnAsn 229  
DB 833 TGGATCCAGAGACATTAAGACAT 859  
RESULT 2  
ID AA222639 standard; cDNA; 1158 BP.  
AA222639  
AC AA222639;  
XX  
AC 08-DEC-1999 (first entry)  
XX  
XX CASB12 derived from Expressed Sequence Tag sequences.  
DE  
XX neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;  
XX autoimmune disease; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH CDS 84..932  
FT /\*tag= a  
FT /product= "CASB12"  
PN WO9949055-A1.  
PD 30-SEP-1999.  
XX  
XX 17-MAR-1999; 99WO-EP001894.  
PF  
XX 20-MAR-1998; 98GB-00006095.  
PR  
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA  
XX Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;  
PI  
XX WPI: 1999-580450/49.  
DR P-PSDB; AAY42440.  
XX  
XX New human serine protease CASB12, for treatment, prevention and diagnosis  
PT of cancer and autoimmune diseases.  
PS Claim 26; Page 49; 58pp; English.  
XX  
XX This is the nucleotide sequence of the CASB12 gene derived from Expressed  
CC sequence tag (EST) search for tumor-specific and tumor-associated  
CC antigens. The nucleotide sequence of AA222638 shows homology with  
CC neuropilin and the encoded protein AAY42439 is structurally related to  
CC other proteins of the serine protease family, having homology and/or  
CC structural similarity with neuropilin. It is expected that as well as  
CC similar structure, these proteins will also share similar biological  
CC functions and properties. The CASB12 polypeptides and polynucleotides can  
CC be used to develop methods for identifying agonists and  
CC antagonists/inhibitors of these molecules, and thereby treating  
CC conditions associated with CASB12 polypeptide imbalance. The invention  
CC also provides for diagnostic assays for detecting diseases associated  
CC with inappropriate CASB12 polypeptide activity or levels. Since CASB12 is  
CC either specifically expressed or highly over-expressed in tumors compared  
CC to normal cells, the polypeptides and polynucleotides of the invention  
CC are believed to be important immunogens for specific prophylactic or  
CC therapeutic immunization against tumors. The polypeptides and  
CC polynucleotides can therefore be targeted by antigen specific immune  
CC reactions (which result in the destruction of the tumor cell) or they can

CC be used to diagnose the occurrence of tumor cells  
 XX  
 SQ Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5,7e-104 Length: 1158  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x AA222639 (1-1158)

QY 1 llellelysglypneglucylslyserprohisserglnproctpglnalaaleupheglu 20  
 Db 243 ATCATCAAGGGGTTGAGTGCAGCCCTCATCCAGCCCTGGCAGGAGCCCTTTCGAG 302  
 QY 21 lvsThrArgLeuLeuCySGlYAlaThrLeuIleAlaProArgTrpLeuThrAla 40  
 Db 303 AAGAGCGGGCTACTCTGTGGGGCAGCCTCATCGCCCCAGATGGCTCTCGACAGCAGCC 362  
 QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysSGlGlu 60  
 Db 363 CACTGCTCTCAAGCCCTGCTACATGTTCTCACTGGGGCAGCACAACCTCCAGAGAGAG 422  
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80  
 Db 423 GGCTGTAGAGCAGACCCGAGACAGCAGTGAAGTCTTCCCCACCCGCTTCAACACAGC 482  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 483 CTCCCAACAAGACCAACCGCAATGACATCATGTGTGAAGATGGATGCCAGCTCC 542  
 QY 101 lIethrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 543 ATCACTCGGGCTGTGGCAACCCCTCAACCTCTCCACAGCTGTGTCACTGCTGGCACAGC 602  
 QY 121 CysLeuLysSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 603 TGCTCTATTCCTGGCTGGGGGAGACCTCCAGCCCTGAGTACGCCCTCCACACCTTG 662  
 QY 141 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 160  
 Db 663 CGATGCCCAATCATCATTGATGACACCAAGAGTGTAGAAGCCCTTACCCCGCAC 722  
 QY 161 lIethrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
 Db 723 ATCAGACAGACCATGTGTGTGGCAGCGTCAAGAGAGGGGGCAAGGACTCTCCAGGGT 782  
 QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln 200  
 Db 783 GACTCCGGGGGCGCTGTGTGTGTGTACAGCTCTTAAAGCATATCTCTGGGGCCAG 842  
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 220  
 Db 843 GATCCGTGTGATCAACCCGAAAGCCTGTGTCTACACGAAATCTGCAAAATGTGGAC 962  
 QY 221 TrpIleGlnGlnThrMetLysAsnAsn 229  
 Db 903 TGGATCCAGAGAGATGAAGAAACAAT 929

RESULT 3  
 ABK92131  
 ID ABK92131 standard; DNA; 1186 BP.

XX AC ABK92131;  
 XX 15-AUG-2002 (first entry)  
 DT Prostate cancer-associated DNA sequence #17.  
 DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
 KW

KW gene therapy; gene; ds.  
 XX Mammalia.  
 OS WO200230268-A2.  
 XX PD 18-APR-2002.  
 XX 12-OCT-2001; 2001US-0288589P.  
 XX 13-OCT-2000; 2000US-00687576.  
 XX 08-DEC-2000; 2000US-00733288.  
 XX 28-DEC-2000; 2000US-00733742.  
 XX 24-JAN-2001; 2001US-0263957P.  
 XX 16-MAR-2001; 2001US-0276791P.  
 XX 16-MAR-2001; 2001US-0276888P.  
 XX 06-APR-2001; 2001US-0281922P.  
 XX 24-APR-2001; 2001US-0286214P.  
 XX 30-APR-2001; 2001US-00847046.  
 XX 04-MAY-2001; 2001US-0288589P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX Gish KC, Mack DH, Wilson KE, Afari D, Hevezi P;  
 XX WPI; 2002-471335/50.  
 XX P-PSDB; AB61816.  
 XX  
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,  
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,  
 PT by determining if prostate cancer-associated genes are expressed in a  
 PT prostate tissue.  
 PT  
 PS Claim 22; Page 313; 436pp; English.  
 XX  
 CC The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated PC genes) that selectively  
 CC hybridize to a sequence that is at least 80% identical to them. The  
 CC prostate cancer-associated polynucleotide sequences are differentially  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.  
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
 CC sequences  
 CC  
 SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5,88e-104 Length: 1186  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x ABK92131 (1-1186)

QY 1 llellelysglypneglucylslyserprohisserglnproctpglnalaaleupheglu 20  
 Db 185 ATCATCAAGGGGTTGAGTGCAGCCCTCATCCAGCCCTGGCAGGAGCCCTTTCGAG 244  
 QY 21 lvsThrArgLeuLeuCySGlYAlaThrLeuIleAlaProArgTrpLeuThrAla 40  
 Db 245 AAGAGCGGGCTACTCTGTGGGGCAGCCTCATCGCCCCAGATGGCTCTCGACAGCAGCC 304  
 QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysSGlGlu 60

Dd		305	CATGGCTCAAGCCCGCTACACTAAGTTCACCTGGGCGACCAACCTCCAGAAGAGAG	364
Qy		61	GlyCysGluGlnThrArgThrAlaThrgIueSerPheProHisProGlyPheAsnSer	80
Dd		365	GGGTGTGAGAGACGCCGGAACGCACCATGTGATCTCCCCACCACCCGGCTTCAACACAGC	424
Qy		81	IeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
Dd		425	CTCCCAACAACAAACACCGCATATGATCTGTGTGAAGATGGATGCCAGTCTCC	484
Qy		101	IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Dd		485	ATCACCTGGGGCTGTGGACCCCTCACCCCTCTCTCCTCACCTGTGTACATGTGGCACACGC	544
Qy		121	CysLeuIleSerGlyTrpPolyserThrSerSerProGlnIleuArgLeuProHisThrLeu	140
Dd		545	TGGCTCATTTCCGGCTGGGGCAGACAGTCCAGCCCCCAGTTACGCTGCTCACACCTTG	604
Qy		141	ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaIleTrpGlyAsn	160
Dd		605	CGATGCCCAACTCATCATCATATTAGACACACGAAAGTGTGAAGACGCTTACCCGGCAC	664
Qy		161	IleThrAspThrValAlaCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly	180
Dd		665	ATCACAGACACCAATGGTGTGTGTGCACGCTGCAGGAAGGGGGCAGAGACTCTGTGCAGAGT	724
Qy		181	AspSerGlyValProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200
Dd		725	GACTCGGGGGCCCTCTGGTCTGTACACAGTCTCTTCAAGCATTAATCTCTGGGGCAG	784
Qy		201	AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp	220
Dd		785	GATCCGGTGCATACACCGAAAGCCTGGTGTCTACAGAAAGTCTGCAAAATATATGTGAC	844
Qy		221	TrpIleGlnIleThrMetLysAsnSer	229
Dd		845	TGATCCAGAGACGATGAAGAACAT	871
<hr/>				
RESULT 4				
ID	ABX76468	standard; DNA; 1186 BP.		
AC	ABX76468;			
XX				
DT	02-APR-2003	(first entry)		
DE				
XX		Lung cancer-associated polynucleotide #332.		
XX				
KM		Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;		
KW		antiinflammatoary; antitachnatic; non-small cell lung cancer; atelectasis;		
KW		small cell lung cancer; benign lesion; precancerous lesion; bronchitis;		
KM		chronic obstructive pulmonary disease; hypersensitivity pneumonitis;		
XX		interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.		
OS		Unidentified.		
XX				
PN	WO200286443-A2.			
XX				
PD	31-OCT-2002.			
PF	18-APR-2002; 2002MO-US012476.			
XX				
PR	18-APR-2001; 2001US-0284770P.			
PR	10-MAY-2001; 2001US-0280492P.			
PR	09-NOV-2001; 2001US-0319245P.			
PR	13-NOV-2001; 2001US-0350666P.			
PR	29-NOV-2001; 2001US-0334370P.			
PR	12-APR-2002; 2002US-0372246P.			
PA	(EOMB-) EOS BIOTECHNOLOGY INC.			
XX				
XX	Aziz N. Murray R;			

XX	WP1: 2003-093161/08.
DR	P-PSDB; ABUS6739.
FR	Detecting a lung cancer-associated transcript in a cell from a patient
PT	for treating lung cancer, by contacting a biological sample from the
PR	patient with a polynucleotide that exhibits increased or decreased
XX	expression in lung cancer.
PS	Claim 22; Page 443; 453pp; English.
XX	The invention relates to a method for detecting a lung cancer-associated
CC	transcript in a cell from a patient, comprising contacting a biological
CC	sample from the patient with a polynucleotide that selectively hybridises
CC	to a sequence that is at least 80 % identical to a gene that exhibits
CC	increased or decreased expression in lung cancer samples. Lung cancer-
CC	associated polynucleotides and polypeptides are used for identifying a
CC	compound that modulates a lung cancer-associated polypeptide, for
CC	inhibiting proliferation of a lung cancer-associated cell to treat lung
CC	cancer in a patient and for treating a mammal having lung cancer by
CC	administering a modulatory compound identified. The methods are useful
CC	for treating lung cancer, such as small cell lung cancer, non-small cell
CC	lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC	emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC	hyperemia/itively pneumonitis, interstitial pulmonary fibrosis, asthma and
CC	bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC	for diagnostic purposes and as targets for screening for therapeutic
CC	compounds that modulate lung cancer, such as antibodies. Sequences
CC	ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC	invention
XX	
SQ	Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other:
XX	
Alignment Scores:	
Pred. NO.:	5,88e-104 Length: 1186
Score:	1258.00 Matches: 229
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DS:	7 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1--229) X ABX76468 (1--1186)	
QY	1 llellelysglpyhedglucylsyprrohisserglnp-ctfpginalaalaleupheglu 20
Db	185 ATCATCAAGGGGTTTCAGTGCAGAAGCTCCTCCAGCGCTTGACGAGGCCCTGTTCAG 244
QY	21 LysThrArgLeuLeuCySGLYAlaThrLeuilealaProArqTLpeLleuThrAlaIa 40
Db	245 AAGACGGGGCTATCTGTGGGGCGACGCTCATCGCCCCCAAGATGCTCTCGACAGCGACC 304
QY	41 HiseryleuuyprokrqgrtylelaHlsleuglygnHlsaeleauGlnySGVlu 60
Db	305 CACGCGCTCAAGCCCGCGTAACATTAGTTACTCTGGGGCACCAACCTCCAGAGAGAGAG 364
QY	61 GLCYsgsluGlInThrArghThAlaThrgJuseRpheProHisPProgilyPheaMenSer 80
Db	365 GGCTGTAGACGACCCGACAGCCACTGAGTCTTCCCACCCCGCTTCACAACAGC 424
QY	81 LeuProAsnlysaSphIsarqsrnsnpillewettlenValysMetAlaserProValSer 100
Db	425 CTCGCCAACAAACACACGCAATAGACATACATGCTGGGAAGAGGCGATGCCAGTCTCC 484
QY	101 lIethTrpAlaValArqProlenuthrleusenSerArqCyVaIltnralaglyThrSer 120
Db	485 ATCACTCGGGCTGTGGACCCCTCAACCCCTCTCAAGCTGTGTACACGTGGCACACAGC 544
QY	121 CysleuileserclyTyTpolySerThrserSerProGlnleuaqlenProHisThleu 140
Db	545 TGCTCTCATTTTCGGCTGGGGCGACAGCTCCACCCCGCTTACCGCTGCTCAACCTTG 604
QY	141 ArgcyvalasnntlethrllleglnHlsGlnyCySGVleualalyPProgilyAsn 160



DB		Prostate cancer marker cDNA.
XX		
KX		Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX		
OS	Homo sapiens.	
XX		
PN	WO2003009814-A2.	
PD		
XX	06-FEB-2003.	
PF		
XX	25-JUL-2002; 2002WO-US023913.	
PR		
XX	25-JUN-2001; 2001US-0307382P	
FR	22-AUG-2001; 2001US-0314356P	
PR	25-SEP-2001; 2001US-0325020P	
PR	12-DEC-2001; 2001US-0341746P	
PR	05-MAR-2002; 2002US-0362158P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
P1	Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbarcheva B;	
P1	Hoersch S, Kamatkar S, Monney AM, Glatt K, Zhao X, Anderson D,	
XX		
XX	WPI; 2003-248033/24.	
PT	New nucleic acid molecule, useful for diagnosing or treating prostate	
PT	cancer.	
XX		
BS	Disclosure; SEQ ID NO 211; 99pp; English.	
XX		
CC	The invention relates to newly discovered cancer markers associated with	
CC	the cancerous state of prostate cells. Also disclosed is a method of	
CC	assessing whether a patient is afflicted with prostate cancer. The method	
CC	of the invention involves assessing whether a patient is afflicted with	
CC	prostate cancer by comparing the level of expression of a marker in a	
CC	patient sample and the normal level of expression of the marker in a	
CC	control non-prostate cancer sample, where a significant increase in the	
CC	level of expression of the marker in the patient sample and the normal	
CC	level indicates that the patient is afflicted with prostate cancer.	
CC	Nucleic acids of the invention are useful for diagnosing or treating	
CC	prostate cancer, and may be useful in gene therapy. Sequences given in	
CC	ADB75177-ADB75611 represent marker cDNA and proteins. Note: The sequence	
CC	data for this patent did not form part of the printed specification, but	
CC	was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
SO	Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 U; 0 Other;	
XX		
	Alignment Scores:	
	Pred. No.: 5,88e-104 Length: 1186	
	Score: 1258.00 Matches: 229	
	Percent Similarity: 100.00% Conservative: 0	
	Best local Similarity: 100.00% Mismatches: 0	
	Query Match: 9 Indels: 0	
	GB: 9 Gaps: 0	
US-09-856-320A-2_COPY_54_282 (1-229) x ADB75387 (1-1186)		
OY	1 llelelrysglyphnegluCysLysProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20	
Db	185 ATCATCAAGGGCTTCATGTGGGGCGACGCATCGGCCCAAGTGGCTCTTACAGCACGC 304	
OY	21 LysThrArgLeuleucySgLyAlaThrLeuIleAlaProArgTrpLeuLeuThraAla 40	
Db	245 AAAGCGGGCTACTCTGTGGGGCGACGCATCGGCCCAAGTGGCTCTTACAGCACGC 304	
OY	41 HisCysLeuLysProArgTrpTyrIleValHisLeuGIyGlnHisAsnLeuGlnLySGlu 60	
Db	305 CACTGGCTCAAGCCCGCGTTCANAGTTCACTCGGGGACGACAACCTCCAAAGAAGAG 364	
OY	61 GlyCYSGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsrSer 80	
Db	365 GGCTGTGAAGAACCCGGAAGCACTGAGTCTTCCCCACCACCCCGGCTTCACAAGAGC 424	

Qy	81	IlePAsnLysAAsPHiSArgHsnAsp11LeuMetLeuValLysMetAlaSerProValSer	100
Db	425	CTCCCAAAAMAAGACCCGCAATACATCATCTGCGTGAAGAGGCGATGCCAGTCTCC	484
Qy	101	IleThrTTPAlaValArgProIeuThrLysSerSerArgCysValThrAlaGlyThrSer	120
Db	485	ATCACTGGGGCTGTGGACCCCTCAACCCCTCTCTCAGCGTGTCTCAGCTGTGGACACG	544
Qy	121	CysLeuIleSerGlyTTPGlySerThrSerSerProGlnIeuAlaGluLeuProHisThrLeu	140
Db	545	TGCTCTATTTCGGCTGGGGCGACAGCTCCAGCCCCAGTTATGCCCTGCTCACACTTG	604
Qy	141	ArgCysAlaAsnIleThrTleIleGlnHisGlnLysCysGluAsnAlaIlyProGlyAsn	160
Db	605	CGATGGCGCAACATCAACATCAATTAGCAGCAGAGAGTGTGAAAGCGCTACCCCGGCAAC	664
Qy	161	IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly	180
Db	665	ATACACACACCATGGTGTGTGTCCAGCGTGCAGAGAGGGGCAAGGACTCTCTGCCAGGT	724
Qy	181	AspSerGlyGlyProIeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln	200
Db	725	GACTCCGGGGGCGCTCTGGTCTGTACACAGCTCTTCCAGGCAATTATCTCTGGGGCAG	784
Qy	201	AspProCysAlaIleThrArgLysProGlyValIlyThrLysValCysLysTlyPValAsp	220
Db	785	GATCCGTGTGCATCACCCGAAAGCGCTGTGTCTTACACGAAAGTCTCCAAATATGTGAC	844
Qy	221	TTPIleGlnGlyThrMetLysAsnAsn	229
Db	845	TGGATCCAGAGACGATGAGAACAT	871
RESULT 7			
AD14842	AD14842 standard; DNA; 1192 BP.		
ID	AD14842		
XX	AA14842;		
AC	01-NOV-2001 (first entry)		
XX	Human PS133 gene contig.		
DE	Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;		
XX	expressed sequence tag; cytosstatic; ds.		
KW	Homo sapiens.		
XX	Location/Qualifiers		
XX	Key		
FT	107..859		
FT	/*tag= a		
FT	/product= "Human PS133 protein"		
FT	/transl_except= (pos:188..196, aa:Cys-Pro)		
FT	/transl_except= (pos:224..232, aa:Phe-Lys)		
XX	US6232456-B1.		
XX	15-MAY-2001.		
PD	06-OCT-1997; 97US-00944483.		
XX	06-OCT-1997; 97US-00944483.		
XX	(ABBO ) ABBOTT LAB.		
PA	Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;		
XX	Russell JC, Stewart KD, Stroupe SD;		
PI	WF; 2001-36357/38.		
XX	P-PSDS; AAB08017.		
DR	New PS133 polynucleotides, useful for detecting, diagnosing, staging,		
XX	monitoring, prognostic, preventing, treating or determining the		





PR 24-SEP-1998; 98US-0101741P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 24-SEP-1998; 98US-0101915P.  
 PR 24-SEP-1998; 98US-0101916P.  
 PR 29-SEP-1998; 98US-0102207P.  
 PR 29-SEP-1998; 98US-0102240P.  
 PR 29-SEP-1998; 98US-0102307P.  
 PR 29-SEP-1998; 98US-0102330P.  
 PR 29-SEP-1998; 98US-0102331P.  
 PR 30-SEP-1998; 98US-0102464P.  
 PR 30-SEP-1998; 98US-0102487P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 30-SEP-1998; 98US-0102571P.  
 PR 01-OCT-1998; 98US-0102684P.  
 PR 01-OCT-1998; 98US-0102687P.  
 PR 02-OCT-1998; 98US-0102965P.  
 PR 06-OCT-1998; 98US-0103258P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 07-OCT-1998; 98US-0103314P.  
 PR 07-OCT-1998; 98US-0103315P.  
 PR 07-OCT-1998; 98US-0103385P.  
 PR 07-OCT-1998; 98US-0103386P.  
 PR 07-OCT-1998; 98US-0103386P.  
 PR 07-OCT-1998; 98US-0103401P.  
 PR 08-OCT-1998; 98US-0103633P.  
 PR 08-OCT-1998; 98US-0103678P.  
 PR 08-OCT-1998; 98US-0103679P.  
 PR 08-OCT-1998; 98US-0103711P.  
 PR 14-OCT-1998; 98US-0104257P.  
 PR 20-OCT-1998; 98US-0104967P.  
 PR 20-OCT-1998; 98US-0105000P.  
 PR 21-OCT-1998; 98US-0105002P.  
 PR 21-OCT-1998; 98US-0105104P.  
 PR 22-OCT-1998; 98US-0105169P.  
 PR 22-OCT-1998; 98US-0105266P.  
 PR 26-OCT-1998; 98US-0105633P.  
 PR 26-OCT-1998; 98US-0105634P.  
 PR 27-OCT-1998; 98US-0105807P.  
 PR 27-OCT-1998; 98US-0105881P.  
 PR 27-OCT-1998; 98US-0105882P.  
 PR 27-OCT-1998; 98US-0106062P.  
 PR 28-OCT-1998; 98US-0106023P.  
 PR 28-OCT-1998; 98US-0106029P.  
 PR 28-OCT-1998; 98US-0106030P.  
 PR 28-OCT-1998; 98US-0106032P.  
 PR 28-OCT-1998; 98US-0106032P.  
 PR 28-OCT-1998; 98US-0106178P.  
 PR 29-OCT-1998; 98US-0106248P.  
 PR 29-OCT-1998; 98US-0106384P.  
 PR 29-OCT-1998; 98US-0108500P.  
 PR 30-OCT-1998; 98US-0106464P.  
 PR 03-NOV-1998; 98US-0106856P.  
 PR 03-NOV-1998; 98US-0106902P.  
 PR 03-NOV-1998; 98US-0106905P.  
 PR 03-NOV-1998; 98US-0106919P.  
 PR 03-NOV-1998; 98US-0106932P.  
 PR 03-NOV-1998; 98US-0106934P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 17-NOV-1998; 98US-0108775P.  
 PR 17-NOV-1998; 98US-0108779P.  
 PR 17-NOV-1998; 98US-0108787P.  
 PR 17-NOV-1998; 98US-0108801P.  
 PR 17-NOV-1998; 98US-0108802P.  
 PR 17-NOV-1998; 98US-0108806P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108807P.  
 PR 17-NOV-1998; 98US-0108925P.  
 PR 18-NOV-1998; 98US-0108848P.  
 PR 18-NOV-1998; 98US-0108849P.  
 PR 18-NOV-1998; 98US-0108850P.  
 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.

PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 XX  
 XX (GENE) GENENTECH INC.  
 XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 PI WPI; 2000-237871/20.  
 DR P-PSDB; AAY99390.  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
 PT PRO polypeptides, useful for screening of potential peptide or small  
 PT molecule inhibitors of the relevant receptor/ligand interactions.  
 XX  
 PS Claim 2; Fig 101; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
 CC primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention  
 XX  
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5,996-104 Length: 1204.  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 3  
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 QY 1 Iletlelysglypnehgucyelysprofhisserglnpctppglnaiaaleupheglu 20  
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 QY 21 LysThrArgLeuLeuCyseGlyAlaThrLeuLeuAlaProArgTrpLeuThraAla 40  
 DB 229 AAGAGCGCGCTACTGTGAGGCGACGCTCACTCGGCCCAATGAGCTCTCAAGCAGC 288  
 QY 41 HisCysLeuysProArgTyrlleValHisleuGlyGlnHisasnleuGlnlyGlu 60  
 DB 289 CACTGCCCTCAAGCCCCCGCTACATGATTCACCTGGGCGAGCAACCTTCAGAGGAG 348  
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisPheAsnAsnSer 80  
 DB 349 GGCTGTGAGCAGACCCGAGCAGCCCTAGTCCTTCCCCCAGCCCGGCTTCAAGCAGC 408  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleWetleuValLysMetAlaSerProValSer 100  
 DB 409 CTCCCAACAAAGACACCGCATGATGCTGCTGGAAGATGCGATCCAGCTCC 468  
 QY 101 IletHrTPAlaValArgProLeuThrLeuSerArgCysValThrAlaGlyThSer 120  
 DB 469 ATCACTGGGCTGTGAGCAGCCCTCACTCTCTCACTGTGTCTGTCTGTGACAGC 528  
 QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 DB 529 TGCCTCATTTCCGGTGGGCGAGCGTCAAGCCCAAGCTTACGCTCTCTCAAGCTT 588  
 QY 141 ArgCysAlaAsnIleThrIleIleleuHisGlnLysCysGlnAsnAlaTyPrpGlyAsn 160  
 DB 589 CGATGGCGCCACATACATCATTTAGACCAAGAGTGTGAGACGGCTTACCCCGGCAAC 648  
 QY 161 IletHrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
 DB 649 ATCAAGACACCATGT 708

QY 161 AsperglyglyProleuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGGCGCTTGGTCTGTACCCAGTCTTCAAGGCATATCTCTCGGGGCGAG 768  
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysIleValAsp 220  
 Db 769 GATCCGGTGGCGATCACCCGAAAGCCTGGTGTACACGAAAGTCTGCAATATGTGGAC 828  
 QY 221 TrpIleGlnGluThrMetLysAsn 229  
 Db 829 TGGATCCAGGAGACGATGAAGAACAT 855  
 RESULT 9  
 AAF54320  
 ID AAF54320 standard; DNA; 1204 BP.  
 AC AAF54320;  
 XX 02-APR-2001 (first entry)  
 DT DNA encoding protein of the invention #51.  
 DE DNA encoding protein of the invention #51.  
 XX Secreted; transmembrane; gene therapy; ss.  
 KM  
 XX Unidentified.  
 OS  
 XX WC0200078961-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 18-FEB-2000; 2000WC-US004342.  
 PF  
 XX 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028513.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WC-US000219.  
 PR 06-JAN-2000; 2000WC-US000376.  
 PA  
 XX (GENTH ) GENENTECH INC.  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams FM, Wood WI;  
 XX WPI; 2001-071395/08.  
 DR  
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX  
 PS Claim 2; Fig 101; 787pp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 CC  
 SQ Sequence 1204 BP; 364 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5,99e-104 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Db: 4 Gaps: 0  
 US-09-856-320A-2\_COPY\_54\_282 (1-229) x AAF54320 (1-1204)  
 QY 1 IleIleLysGlyPheGlyCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
 Db 169 ATCATCAAGGGGTTGATGCAAGCTCACTCCAGCCCTGGACAGCGACCTGTTCGAG 228  
 QY 21 LysThrArgLeuLeuCysGlyValAlaThrIleuIleAlaProArgTrpLeuThrAla 40  
 Db 229 AAGACGGCGTACTCTGTGGGGCGAGCGCTCACTCGCCCAAGATGGCTCTCGACACAGCC 288  
 QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60  
 Db 289 CACTGCTCAAGCCCGCTACATAGTCACTGGGGGCGACACACTCCAGAGGAGAG 348  
 QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80  
 Db 349 GGGTGTGAGCAGACCCCGGACAGCCCACTAGTCTTCCCCACCCCGGCTTCAACACAGC 408  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 Db 409 CTCCCAACAAAGACACCGCATATCATAGTGTGGAGATGGCATCGCCAGTCTCC 468  
 QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
 Db 469 ATCACTGGGGCTGTGCGACCCCTCACTCTCTCTACCGTGTGTACTGTGGCACAGC 528  
 QY 121 CysIleuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
 Db 529 TGCCTCATTTCCGGCTGGGGGCGACAGCTGCAGCCCGCCAGTTAAGCTCTCTCACACCTTG 588  
 QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaIleTrpProGlyAsn 160  
 Db 589 CGATCGGCCAATATCAATCATTTAGACACCAAGATGTGAAGACCTTACCCCGGACAC 648  
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
 Db 649 ATCACAGACACCATGTGTGTGCCAGCGTGCAGAGGGGGAAGGACTCTCTGCCAGGCT 708  
 QY 181 AsperglyglyProleuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
 Db 709 GACTCCGGGGGCGCTTGGTCTGTACCCAGTCTTCAAGGCATATCTCTCGGGGCGAG 768  
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysIleValAsp 220  
 Db 769 GATCCGGTGGCGATCACCCGAAAGCCTGGTGTACACGAAAGTCTGCAATATGTGGAC 828  
 QY 221 TrpIleGlnGluThrMetLysAsn 229  
 Db 829 TGGATCCAGGAGACGATGAAGAACAT 855  
 RESULT 10  
 AAS21496  
 ID AAS21496 standard; cDNA; 1204 BP.  
 XX  
 AC AAS21496;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT  
 DE Human cDNA sequence encoding for PRO1279 polypeptide.  
 XX  
 XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WC0200140466-A2.

07-JUN-2001.  
 01-DEC-2000; 2000WO-US032678.  
 01-DEC-1999; 99WO-US028301.  
 01-DEC-1999; 99WO-US028634.  
 02-DEC-1999; 99WO-US028551.  
 02-DEC-1999; 99WO-US028564.  
 02-DEC-1999; 99WO-US028565.  
 09-DEC-1999; 99US-0170282P.  
 16-DEC-1999; 99WO-US030095.  
 20-DEC-1999; 99WO-US030911.  
 20-DEC-1999; 99WO-US030999.  
 30-DEC-1999; 99WO-US031243.  
 30-DEC-1999; 99WO-US031274.  
 05-JAN-2000; 2000WO-US000219.  
 06-JAN-2000; 2000WO-US000277.  
 06-JAN-2000; 2000WO-US000376.  
 11-FEB-2000; 2000WO-US003565.  
 18-FEB-2000; 2000WO-US004341.  
 18-FEB-2000; 2000WO-US004342.  
 22-FEB-2000; 2000WO-US004414.  
 24-FEB-2000; 2000WO-US004514.  
 24-FEB-2000; 2000WO-US005004.  
 01-MAR-2000; 2000WO-US005501.  
 02-MAR-2000; 2000WO-US005841.  
 03-MAR-2000; 2000US-0187202P.  
 10-MAR-2000; 2000WO-US006319.  
 15-MAR-2000; 2000WO-US006884.  
 20-MAR-2000; 2000WO-US007377.  
 21-MAR-2000; 2000WO-US007532.  
 30-MAR-2000; 2000WO-US008439.  
 17-MAY-2000; 2000WO-US013705.  
 22-MAY-2000; 2000WO-US014042.  
 30-MAY-2000; 2000WO-US014941.  
 02-JUN-2000; 2000WO-US015264.  
 05-JUN-2000; 2000US-0209832P.  
 28-JUL-2000; 2000WO-US020710.  
 11-AUG-2000; 2000WO-US020311.  
 23-AUG-2000; 2000WO-US023522.  
 24-AUG-2000; 2000WO-US023328.  
 08-NOV-2000; 2000WO-US030952.  
 10-NOV-2000; 2000WO-US030873.  
 (GENTH ) GENENTECH INC.  
 Baker KP, Barresini M, DeForge L, Desnoyers J, Filvaroff E, Gao W, Gerriksen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2001-408281/43.  
 P-PSDB; AAU12424.  
 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.  
 Claim 3; Fig 505; 813pp; English.  
 AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes

(PEMWS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide to factor VIIa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	5.99e-104	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x AAS21496 (1-1204)

QY	1	IleIleIleYsgIyPhneIuCyAlpProHisSerGlnProTrrpGlnAlaIleuPhneIu	20
DB	169	ATCATCAAGGAGGATTGAGTGCAGACCTCCAGCCCTGGCAGGACGCTTGTTCAG	228
QY	21	LysThrArgLeuLeuCyGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla	40
DB	229	AAGAGCGCGCTACTCTGTGGGCGAGCGTCAACCCCAATGGCTCTTCAGCAGACC	288
QY	41	HisCysLeuYsProArgTyrIleValHisLeuIyGlnHisAsnLeuGlnYsgIu	60
DB	289	CACCTCCCTCAAGCCCGGCTCATAGTTCACCTGGGCGAGCAACCTCCAGAGAGAG	348
QY	61	GlyCysGlnGlnThrArgThrAlaThrGlnSerThrProHisProGlyIleAsnSer	80
DB	349	GGCTGTGAGCAGACCCGAGCAGCCAGTGAAGCTTCCCAACCCCGGCTTAAACAAC	408
QY	81	LeuProAsnYsAspHisArgAsnAspIleMetLeuValYsMetAlaSerProValSer	100
DB	409	CTCCCAACCAAGACCAACCGATGACATCTGCTGGAGAGATGGCATGGCAGTCTCC	468
QY	101	IleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThrSer	120
DB	469	ATCACCTGGGCTGTGCGACCCCTCAACCTCTCCACCTGTGTACGTGCTGGCAGAC	528
QY	121	CysLeuIleSerGlyThrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
DB	529	TGCTTCATTTCCGCTGGGCGAGCGACGTCAGCCCGGATTAAGCTTCCTCAGCCTTG	588
QY	141	ArgCysAlaAsnIleThrIleIleGlnHisGlnYsCysGlnAsnAlaTyrProGlyAsn	160
DB	589	CGATGGCGCAACATCACCATTGAGCAGCAGAAAGTGTGAAAGCGCTTACCCGCGAAC	648
QY	161	IleThrArgThrMetValCysAlaSerValGlnGlnYsgIyYsAspSerCysGlnGly	180
DB	649	ATCACAGACACCATGTGTGTGCGAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGG	708
QY	181	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln	200
DB	709	GATCCGGGGGCGCCCTGTGTGTGTAACAGCTCTTCAAGCATATCTCTGGGGCGAG	768
QY	201	AspProCysAlaIleThrArgLysProGlyValTyrThrIleValCysLysTyrValAsp	220
DB	769	GATCCGTGGCATCAGCCGGAAGCGTGTGTCTACAGAAAGTGTGCAAAATGTGTGAC	828
QY	221	TrpIleGlnGlnThrMetLysAsnAsn	229
DB	829	TGATTCAGAGAACATGAAAGCAAT	855

RESULT 11  
 ABEK33628 standard; cDNA; 1204 BP.  
 ID ABEK33628  
 AC ABEK33628;

XX 08-MAY-2002 (first entry)  
DT  
XX  
CC CDNA encoding human PRO protein, Seq ID No 185.  
DE  
XX  
KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KM breast cancer; prostate tumour; rectal tumour; liver tumour;  
KM pericyte cell proliferation; chondrocyte cell proliferation;  
KM tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
XX 29-JUN-2001; 2001WO-US021066.  
XX  
PP 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220585P.  
PR 25-JUL-2000; 2000US-0220605P.  
PR 25-JUL-2000; 2000US-0220607P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220638P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 25-JUL-2000; 2000US-0220666P.  
PR 26-JUL-2000; 2000US-0220893P.  
PR 26-JUL-2000; 2000WO-US020710.  
PR 01-AUG-2000; 2000US-0222425P.  
PR 22-AUG-2000; 2000US-0227133P.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 28-NOV-2000; 2000US-0253646P.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854288.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
XX WPI; 2002-172001/22.  
DR P-PSDB; AAU83684.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumors such  
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
PT or liver tumor.  
XX  
XX Claim 2; Fig 185; 359bp; English.  
PS  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
CC liver tumor. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes.

CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO  
CC protein coding sequences of the invention  
XX  
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 5,99e-104 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-320A-2\_COPY\_54\_282 (1-229) x ABK33628 (1-1204)  
QY 1 IleIleIleGlyPheGluCysLysProHisSerGlnProTyrGlnAlaIleLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTCAGTGAAGCTCACTCCAGCCCTGGACAGCAGCCTGTTGAG 228  
QY 21 LysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTyrLeuThrAlaAla 40  
DB 229 AAGACCGGCTACTCTGTGGGGGAGCGCTCATGCCCCCAGATGGCTCTGACAGAGCC 288  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60  
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGACACACCTCCAGAGAGAGG 348  
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GGCTGTGACAGACCGCGACAGCCACTGAGTCTTCCCCACCCGGCTTCAACAGAGC 408  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValIleMetAlaSerProValSer 100  
DB 409 CTCGCCAAGAGACACCGCCATCATCATCATCATCATCATCATCATCATCATCATCAT 468  
QY 101 IleThrTyrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 528  
QY 121 CysLeuIleSerGlyTyrProLysSerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 529 TGCTCATTTCCGGCTGGGGGAGCAGCTCACCCCACTTACGGCTGCTCACACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 589 CGATCGCCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerGlyGlnGly 180  
DB 649 ATCAACAGACACCATGTGTGTGTCACCGTGCAGAGAGGGGCAAGACATCCGCCAGGT 708  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200  
DB 709 GATTCGGGGGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768  
QY 201 AspProCysAlaIleThrArgLysProGlyValIlyThrLysValCysLysTyrValAsp 220  
DB 769 GATCCGCTGTGCATCACCCGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 828  
QY 221 TrrIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCAGAGAGCATGAGAGACANT 855  
RESULT 12  
AB188175  
ID AB188175 standard; CDNA; 1204 BP.  
XX  
AC AB188175;  
XX  
XX 16-MAY-2002 (first entry)  
DT  
XX  
XX Human PRO1279 CDNA sequence SEQ ID NO:207.  
XX

Human; angiogenesis; cardiant; cyostatic; antiangiogenic; hypotensive;  
vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hyperextension;  
age-related macular degeneration; arterial restenosis; angina;  
rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US019692.  
XX  
XX 23-JUN-2000; 2000US-0213637P.  
XX 20-JUL-2000; 2000US-0219556P.  
XX 25-JUL-2000; 2000US-0220624P.  
XX 28-JUL-2000; 2000US-0220664P.  
XX 02-AUG-2000; 2000US-02220710.  
XX 17-AUG-2000; 2000US-0222695P.  
XX 23-AUG-2000; 2000WO-US023522.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 07-SEP-2000; 2000US-023078P.  
XX 18-SEP-2000; 2000US-00664610.  
XX 18-SEP-2000; 2000US-00665530.  
XX 24-OCT-2000; 2000US-0242922P.  
XX 08-NOV-2000; 2000US-00709238.  
XX 08-NOV-2000; 2000WO-US030952.  
XX 10-NOV-2000; 2000WO-US030873.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 20-DEC-2000; 2000US-00747259.  
XX 20-DEC-2000; 2000WO-US034956.  
XX 22-JAN-2001; 2001US-00767609.  
XX 28-FEB-2001; 2001US-00796498.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 01-MAR-2001; 2001WO-US006566.  
XX 09-MAR-2001; 2001US-00802706.  
XX 14-MAR-2001; 2001US-00808689.  
XX 22-MAR-2001; 2001US-00816744.  
XX 05-APR-2001; 2001US-00828366.  
XX 10-MAY-2001; 2001US-00854208.  
XX 10-MAY-2001; 2001US-00854280.  
XX 25-MAY-2001; 2001US-00866028.  
XX 25-MAY-2001; 2001US-00866034.  
XX 25-MAY-2001; 2001WO-US017092.  
XX 30-MAY-2001; 2001US-00870574.  
XX 30-MAY-2001; 2001WO-US017443.  
XX 01-JUN-2001; 2001WO-US017800.  
XX  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,  
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
XX Stephan WF, Watanabe CK, Williams PM, Wood WI, Ye W,  
XX  
XX WPI: 2002-090516/12.  
XX P-PSDB: ABB84920.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX Claim 2; Fig 207; 565pp: English.  
XX  
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,  
XX antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic  
XX activities, and can be used in gene therapy. The PRO polynucleotides,  
XX proteins, agonists and antagonists are useful for treating or diagnosing

a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
healing. The PRO polynucleotides have applications in molecular biology,  
including use as hybridisation probes, and in chromosome and gene  
mapping. ABL88259 to ABL88267 represent primers and probes used in the  
exemplification of the present invention

XX  
XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 5,99e-104 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-856-320a-2\_COPY\_54\_282 (1-229) x ABL88175 (1-1204)  
QY 1 ILEILEYGLYPHEGLUCYLSYFROHISSEGINPOTTPGINAIAALEUPHEGLU 20  
DB 169 ATCATCAAGGGGTTGAGTGCAGGCTCACCAGCCCTGGAGGAGCCCTGTGAG 228  
QY 21 IYSTRARGLEULEUCYGLYALATHREULEALAPROAGTTPLEULETHALALA 40  
DB 229 AAGACGCGACTACTCTGCGGCGACGCTCACGCCCCAAGAGCTCTTACGCGACC 288  
QY 41 HISCYLSLEULYSPROAGTYRILEVALHISLEUGLYINHISANLEUGLISGLUGLU 60  
DB 289 CACTGCCCTCAAGCCCGCGTATAGTTCACTGGGGGAGCACAACCTCCAGAGAGAG 348  
QY 61 GLYCYGLUGLINTHARGTHALATHRGLEUSERPHEPHOHISPROGLYPHASANSE 80  
DB 349 GGCTGTGACAGACCCGACAGCCACGCTAGCTCTCCGCCGCCGCTTAAACAGAC 408  
QY 81 LEUPROANLYSASPHEARGASNPILVECTLEUVALLYSMETALASERPROVALSER 100  
DB 409 CTCGCCAACAAGACCAACCGCATATCATGTGCTGGAGAGAGGATGCCAGTCTCC 468  
QY 101 ILEHTTPALAVALAYPROLEUTHREUSERSEARGLCYVALTHRALGLYTHSER 120  
DB 469 ATCACTGGGGCTGTCGACCCCTCCCTCCCTCCCTGTCACCTGTGCACGCGACAC 528  
QY 121 CYLSLEULESERGLYTPGLYSETHREUSERSEARGLCYVALTHRALGLYTHSER 140  
DB 529 TCCCTCATTTCCGCTGGGGGACGACGTCGCCGCCGCCGTTACCCCTCACACCTG 588  
QY 141 ARGCYSLAASNIETHTLEILEGILHISGLINLYSCYGIUAMALATYRPROGLYASN 160  
DB 589 CGATCGCCCAACATCACCATTAGACACCAAGTGTGAGAACGCTTACCCCGGCAC 648  
QY 161 ILEHTRAPPTHTMERVALCYSLASERVALGLINGLUGLYLYSASPSECYSGILGLY 180  
DB 649 ATCAACAGACACCATGTGTGTGCCGCTGACGAGAGGGGCAAGAGATCTGCCAGG 708  
QY 181 ASPSERGLYGLYPROLEUVALCYSANGLINSEIRLEUGLINGLYILESESTTPGLYGLN 200  
DB 709 GACTCGGGGGGCGCTCTGTGTGTAACCAAGCTCTTCAAGGCAATTATCTGGGGCAG 768  
QY 201 AAPPROCYSAIAILETHARGLYSEPROGLYVALYTHIRLYSVALCYSLYTYVALASP 220  
DB 769 GATCCGTGTGCGATCACCCGAAAGCTGTGTCTACAGAAAGTGTGCAATATGTGAGC 828  
QY 221 TTPILGLINGLUTHMETLYSASN 229  
DB 829 TGGATCCAGAGACGATGAGACAT 855  
RESULT 13  
ABL95664  
ID ABL95664 standard; cDNA; 1204 BP.

AC ABL95664;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208284-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 09-JUL-2001; 2001WO-US021735.  
 XX  
 PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 02-AUG-2000; 2000US-0222595P.  
 PR 17-AUG-2000; 2000US-0064557.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 07-SEP-2000; 2000US-0230378P.  
 PR 18-SEP-2000; 2000US-00654610.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 10-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-0074259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00815744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-0086028.  
 PR 25-MAY-2001; 2001US-0086034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PA (BAKE ) BAKER K P.  
 PA (FERE ) FERRARA N.  
 PA (GERB ) GERBER H.  
 PA (GERR ) GERRITSEN M E.  
 PA (GODD ) GODDARD A.  
 PA (GODO ) GODOWSKI P J.  
 PA (GUNE ) GURNEY A L.  
 PA (HILL ) HILLAN K J.  
 PA (MARS ) MARSTERS S A.  
 PA (PANU ) PAN J.  
 PA (PAON ) PAONI N F.  
 PA (STEP ) STEPHAN J F.  
 PA (WATA ) WATANABE C K.  
 PA (WILL ) WILLIAMS P M.  
 PA (WOOD ) WOOD W I.  
 XX

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 DR WPI: 2002-171999/22.  
 DR P-PSDB; ABB95526.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 1, Fig 207; 567pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention  
 XX  
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5,99e-104 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
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US-09-856-320A-2\_COPY\_54\_282 (1-229) X ABL95664 (1-1204)

QY 1 IletlelysglypneghluCyseLyseProHiseSerGlnProTPGlnAlaIalaPheghlu 20  
 DB 169 ATCATCAAGGGGTTGAGTGAAGCTCACCCTCCAGCCCTTGCGAGGAGCCCTTTGAG 228  
 QY 21 LysThrArgLeuLeuCyseGlyAlaThrIleuAlaProArgTPLeuLeuThAlaAla 40  
 DB 229 AAGACGGCGTACTGTGTGGGGCGACGCTCATCCGCCAGATGGCTTCACAGCAGCC 288  
 QY 41 HisCysLeuLysProArgTPYrIleValHisIleuGlyGlnHisAsnLeuGlnYsglu 60  
 DB 289 CACTGCTCAAGCCCGCTACATATGTTCTGAGGGAGGACCAACCTCCAGAAAGAGGAG 348  
 QY 61 GlyCysGlnGlnThrArgThAlaThrGlySerPheProHisProGlyPheAsnAsnSer 80  
 DB 349 GCGTGTGAGCAGACCCGAGACGACCTGAGTCTCCGCCAGCCGCTTCAACACAGC 408  
 QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
 DB 409 CTCCCAACAAAGACACCGCAATGACATCATGCTGTGAGAGTGGATGCGCAGTCTCC 468  
 QY 101 IleThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThAlaGlyThSer 120  
 DB 469 ATCACTGGGCTGTGCAACCCCTCACCCCTCCCTCAGCGTGTGCACTGCTGGACACAGC 528  
 QY 121 CysIleuIleSerGlyTPGlySerThSerSerProGlnLeuArgLeuProHisfThLeu 140  
 DB 529 TGCCCTCATTTCCGGCTGGGGGAGACGTCACAGCCGCCAGTTACCCCTGCTCACACCTTG 588  
 QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTPYrProGlyAsn 160  
 DB 589 CGATGGCCCAACATCATCATATTGAGCACCAGAAAGTGTAGAACGCTTACCCCGGACAC 648  
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyIleGlyLysAspSerCysGlnGly 180  
 DB 649 ATCAACAGACACCATGTGTGTGTGACAGCGTGCAGAGAGGGGCAAGAGCACTCTCCAGGGT 708  
 QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTPGlyGln 200  
 DB 709 GACTCCGGGGGCGCTCTGTGTGTGTGTAACCATGCTCTTCAAGCATATTCTCTTGGGGCAG 768

QY 201 AspProCysAlaIleThraArgLysProGlyValIleThraLysValCysLysIleValAsp 220  
DB 769 GATCGCTGCGATACCCGAAAGCCTGATGCTTACACGAAAGTGTGCAAAATATGTGAC 828  
QY 221 TPTLEGLingIuThreLysAsn 229  
DB 829 TGGATCCAGAGCGATGAAGAACAT 855

RESULT 14  
ACD24105  
ID ACD24105 standard; cDNA; 1204 BP.  
XX  
AC ACD24105;  
XX  
DT 26-AUG-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1279 cDNA.  
XX  
XX Human; secreted and transmembrane protein; PRO; antiinflammatory;  
XX antiarteriosclerotic; cardiact; anti-infectility; anti-HIV; cytostatic;  
XX antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
XX TNF-alpha release; cell proliferation; cell differentiation;  
XX gene expression modulator; proteoglycan release; atherosclerosis;  
XX tumour; inflammatory disease; organ failure; premature aging; AIDS;  
XX cardiac injury; infectility; birth defect; prematurity; cancer; diabetic complication;  
XX acquired immunodeficiency syndrome; cancer; diagnostic; biosensor;  
XX chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
XX bioreactor; tissue typing; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX US2003032156-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 06-MAY-2002; 2002US-00140474.  
XX  
XX 31-MAR-1997; 97WO-US005230.  
XX 12-JUN-1998; 98WO-US012456.  
XX 14-JUL-1998; 98WO-US014552.  
XX 28-AUG-1998; 98WO-US017888.  
XX 10-SEP-1998; 98WO-US018824.  
XX 14-SEP-1998; 98WO-US019893.  
XX 14-SEP-1998; 98WO-US019094.  
XX 14-SEP-1998; 98WO-US019177.  
XX 16-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 17-SEP-1998; 98WO-US021141.  
XX 29-OCT-1998; 98WO-US022991.  
XX 29-OCT-1998; 98WO-US022992.  
XX 29-OCT-1998; 98WO-US024855.  
XX 01-DEC-1998; 98WO-US025108.  
XX 05-JAN-1999; 99WO-US000106.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99WO-US005190.  
XX 20-APR-1999; 99WO-US008615.  
XX 14-MAY-1999; 99WO-US010733.  
XX 02-JUN-1999; 99WO-US012252.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
XX 13-SEP-1999; 99WO-US020944.  
XX 15-SEP-1999; 99WO-US021090.  
XX 15-SEP-1999; 99WO-US021547.  
XX 05-OCT-1999; 99WO-US023089.  
XX 29-NOV-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
XX 30-NOV-1999; 99WO-US028409.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028554.  
XX 02-DEC-1999; 99WO-US028555.  
XX

PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005801.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006665.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 05-JUN-2001; 2001WO-US017800.  
PR 14-JUN-2001; 2001US-00874503.  
PR 19-JUN-2001; 2001US-00882636.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927936.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
XX Pi Gerritsen ME, Goddard A, Godowski PJ, Gurney AJ, Sherwood S,  
XX Pi Smith V, Stewart TA, Tumas D, Watanabe CX, Wood WT, Zhang Z,  
XX WPI; 2003-34180/32.  
XX P-PSDB; ABO17868.



XX New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, acquired immunodeficiency  
PT syndrome (AIDS), or cancer.

XX Claim 2; Fig 505; 660pp; English.

XX The invention describes an isolated nucleic acid (I) comprising, or which  
CC has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences  
CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumor necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This sequence encodes a novel human secreted and transmembrane PRO  
CC polypeptide

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	Score:	Length:
1258-104	1258.00	229
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatch: 0
Query Match:	100.00%	Indels: 0
DB:	7	Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x ACD24105 (1-1204)

QY 1 Ilelelysglyphegiucyslyspriohisserglnprotrpqlalalaaleuphegiu 20  
DB 169 ATCATCAAGGGGTGAGTGCAGCTCACTCCAGCCCGAGGAGAGCCCTGTCGAG 228  
QY 21 lyethrhrgrleuencysglvalaathleuleala1prohrgtrpneuutrralaala 40  
DB 229 AAGACGGGCTACTCTGTGGGCGACCTCATCGCCCGCATGAGTCTCGACAGAGCC 288  
QY 41 HisCysleuysproargtyrlievalhisleuglyhishisnleuglnysgiu 60  
DB 289 CAGTGGCTCAAGCCCGCTCATAGTTCACCTGGGAGACACAACCTCGAAGAGAGAG 348  
QY 61 GlyCysgluIntrrargthrra1aThrGluserPheprohishproglipheananser 80  
DB 349 GGGCTAGAGAGAGCCGAGAGAGCCATGAGTCTCTCCCAACCCCGCTTCAACAAGAGC 408  
QY 81 leuprpsanlysaaphisargasnaaspillemetleuvalysmetlaserprovalser 100  
DB 409 CTCGCCAACAAGACCAACCCCAAGATCATGTGTGTAAGATGGATGCCAGTCTCC 468  
QY 101 l1ethrtrpalaVala1pProleuThleuSerserArgCysValThra1aglyThrser 120  
DB 469 ATCACCTGGGCTGTGCAACCCCTCATACCTCTCCCAAGCTGTCTCATCTGTGCACAGC 528  
QY 121 CysleuilesergytYrpglyserThrserserproglinleuargleuprohisThrleu 140  
DB 529 TGCTTCATTTCCGCTGGGAGAGAGCTCCAGCCCAAGTTACCCCTGCTCACACTTG 568  
QY 141 ArgCysalaalaenilethr1leleleghisglinysCysgluanaala1YrproglYasn 160

DB 589 CGATCGGCCAATCACCATGATGAGCACCAGAAAGTGTAGAAAGCCTACCCCGGCAAC 648  
QY 161 l1ethrhrpThrMetValCysAlaSerValInglu1glYlysaSpserCtyglInglY 180  
DB 649 ATCACAGACACCATGTGTGTGCGAGCGTGCAGAGAGGGGAGAGACTCTGTCAGAGGT 708  
QY 181 AspSerGlyglYpProleuValCysasn1nserleugln3lyle1leSerTrpGlyGln 200  
DB 709 GACTCCGGGGGCCCTCTGTGTGTACCAAGTCTTCAAGCATTAATCTCTGGGGCCAG 768  
QY 201 AspProCysAla1leThraXlyspProglYVal1YrThlyValCyslyeTyValasp 220  
DB 769 GATCGGTGTGCATCACCAGAAAGCTGTGTCTACAGAAAGCTGTGCAATATGTGTGAC 828  
QY 221 Trp1leGln1uThrMetLysAsn 229  
DB 829 TGGATCCAGAGAGCATGAGAACAT 855

#### RESULT 15

ACAA66933 standard; CDNA; 1204 BP.

ACAA66933;

23-JUN-2003 (first entry)

CDNA encoding human PRO polypeptide #93.

Human; PRO polypeptide; secreted and transmembrane protein;

anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic;

gene; ss.

Homosapiens.

US2003036635-A1.

20-FEB-2003.

28-AUG-2002; 2002US-00230163.

25-JUL-2000; 2000US-0220638P.

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US021066.

09-APR-2002; 2002US-00119480.

(GENTH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,

Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,

WPI; 2003-342045/32.

P-PSDB; AB080831.

One hundred and twenty two nucleic acids encoding PRO polypeptides,

tumor.

Claim 2; Fig 185; 314pp; English.

The present invention relates to the isolation of novel human PRO

polypeptides, and the polynucleotide sequences encoding them. The PRO

polypeptides are secreted and transmembrane proteins. The PRO

polypeptides and polynucleotides are useful for preparing a medicament

useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are

useful in diagnostic assays for PRO, by detecting its expression in

specific cells, tissues or serum, and for affinity purification of PRO

from recombinant cell culture or natural sources. ACAA66841-ACAA66962

represent CDNA sequences encoding the human PRO polypeptides of the

invention. Note: The sequence data for this patent was obtained in

CC electronic format directly from the USPTO web site at

segdata.uspto.gov/psipsideentity.html

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	5,99e-104	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x ACA66933 (1-1204)

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DB      169 ATCATCAAGGGGCTCGAGTCAGCCCTCACTCCCAAGCCCTGGCAGCGAGCCCTGTCGAG 228
QY      21  LyethrArgleuLeuCySGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
DB      229 AAGACGGGGCTACTCTGTGGGGCGACGCTCATGCCCCCAATGGCTCTCTGACAGAGGCC 288
QY      41  HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysglu 60
DB      289 CACTGCTCAAGCCCGCTCATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGAGAGAG 348
QY      61  GlyCysgluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
DB      349 GGCCTGAGCAGACCCGAGACAGCCACAGTCTTCCCAAGCCGCTTCAACCAACAGC 408
QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB      409 CTCGCCAACAAGACCAACCGCAATGACATCATGTGTTGAAGATGGCATGGCCAGTCTCC 468
QY      101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB      469 ATCACTGGGCTGTGGCAGCCCTCACCCCTCTCTCAAGCTGTGTCACTGTGGCAGCAGC 528
QY      121 CysLeuLysSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB      529 TGCTCTATTTCGGGCTGGGGCAGCAGCTCCAGCCCCCAAGTTACGCTGCTCAGACCTTG 588
QY      141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyProGlyAsn 160
DB      589 CGATGCCGCCAACAATCACCATCATGAGCACAGAAAGTGAAGAACGCTACCCCGGCAAC 648
QY      161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB      649 ATCAAGAGACCATGAGTGTGTGCGAGGTCAGAGAGGGGCAAGGACTCTCTCCAGGGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB      709 GACTCCGGGGGCCCTGTGTCGTGAACCAAGTCTCTTCAAGGCATTAATCTCTGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValIleTyThrLysValCysLysTyValAsp 220
DB      769 GATCCGTGTGCGATCAGCCCAAGCCCTGTGTCTACACGAAAGTGTGCAAAATATGTGAGC 828
QY      221 TrpIleGlnGluThrMetLysAsnAsn 229
DB      829 TGAATCCAGAGAGATGAAGAACAAT 855

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Search completed: June 23, 2004, 01:43:24  
 Job time : 463 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: June 23, 2004, 01:35:34 ; Search time 469 Seconds  
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2236.822 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
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Sequence:

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Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0  
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Post-processing:

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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No. Score Match Length DB ID

Description

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2	1258	100.0	1186	16	US-10-805-823-211	Sequence 211, App
3	1258	100.0	1186	15	US-10-295-027-559	Sequence 559, App
4	1258	100.0	1186	16	US-10-173-999-159	Sequence 159, App
5	1258	100.0	1204	10	US-09-946-374-169	Sequence 169, App
6	1258	100.0	1204	12	US-10-015-395A-169	Sequence 169, App
7	1258	100.0	1204	13	US-10-147-493-505	Sequence 505, App
8	1258	100.0	1204	13	US-10-145-127-505	Sequence 505, App
9	1258	100.0	1204	13	US-10-160-503-505	Sequence 505, App
10	1258	100.0	1204	13	US-10-143-118-505	Sequence 505, App
11	1258	100.0	1204	13	US-10-144-993-505	Sequence 505, App
12	1258	100.0	1204	13	US-10-158-787-505	Sequence 505, App
13	1258	100.0	1204	13	US-10-081-056-207	Sequence 207, App
14	1258	100.0	1204	13	US-10-219-535-185	Sequence 185, App
15	1258	100.0	1204	13	US-10-232-230-185	Sequence 185, App
16	1258	100.0	1204	13	US-10-140-024-505	Sequence 505, App
17	1258	100.0	1204	13	US-10-140-808-505	Sequence 505, App
18	1258	100.0	1204	13	US-10-006-485A-169	Sequence 169, App
19	1258	100.0	1204	13	US-10-013-907A-169	Sequence 169, App
20	1258	100.0	1204	13	US-10-015-499A-169	Sequence 169, App
21	1258	100.0	1204	13	US-10-232-224-185	Sequence 185, App
22	1258	100.0	1204	13	US-10-152-405-505	Sequence 505, App
23	1258	100.0	1204	13	US-10-127-852A-505	Sequence 505, App
24	1258	100.0	1204	13	US-10-127-900A-505	Sequence 505, App
25	1258	100.0	1204	13	US-10-126-685A-505	Sequence 505, App
26	1258	100.0	1204	13	US-10-226-254A-169	Sequence 169, App
27	1258	100.0	1204	13	US-10-131-820A-505	Sequence 505, App
28	1258	100.0	1204	13	US-10-142-886-505	Sequence 505, App
29	1258	100.0	1204	13	US-10-146-128-505	Sequence 505, App
30	1258	100.0	1204	13	US-10-146-786-505	Sequence 505, App
31	1258	100.0	1204	13	US-10-147-459-505	Sequence 505, App
32	1258	100.0	1204	13	US-10-157-798-505	Sequence 505, App
33	1258	100.0	1204	13	US-10-305-654-207	Sequence 207, App
34	1258	100.0	1204	15	US-10-028-072-505	Sequence 505, App
35	1258	100.0	1204	15	US-10-121-049-505	Sequence 505, App
36	1258	100.0	1204	15	US-10-123-904-505	Sequence 505, App
37	1258	100.0	1204	15	US-10-140-470-505	Sequence 505, App
38	1258	100.0	1204	15	US-10-175-746-505	Sequence 505, App
39	1258	100.0	1204	15	US-10-176-921-505	Sequence 505, App
40	1258	100.0	1204	15	US-10-176-921-505	Sequence 505, App
41	1258	100.0	1204	15	US-10-227-884-185	Sequence 185, App
42	1258	100.0	1204	15	US-10-137-865-505	Sequence 505, App
43	1258	100.0	1204	15	US-10-140-474-505	Sequence 505, App
44	1258	100.0	1204	15	US-10-142-431-505	Sequence 505, App
45	1258	100.0	1204	15	US-10-143-114-505	Sequence 505, App

## ALIGNMENTS

RESULT 1  
US-10-240-425-349  
Sequence 349, Application US/10240425  
Publication No. US20040033502A1  
GENERAL INFORMATION:  
APPLICANT: Williams, Amanda  
APPLICANT: Boland, Joseph F.  
APPLICANT: Lord, Reginald V.  
APPLICANT: Alvarez, Chris  
APPLICANT: Metzel, Jon C.  
APPLICANT: Schert, Uwe  
APPLICANT: Vockley, Joseph G.  
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
FILE REFERENCE: 44921-5026  
CURRENT APPLICATION NUMBER: US/10/240,425  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: PCT/US01/09847  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 60/193,446  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ IDS: 1588  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 349

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/ LENGTH: 1186
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US2004003502A1 AB012917
US-10-240-425-349

Alignment Scores:
Pred. No.: 4.2e-142      Length: 1186
Score: 1258.00          Matches: 229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 13                  Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-240-425-349 (1-1186)

QY 1 IletlelySGlyPheGluCyslySProHisSerGlnProTPGlnAlaLeuPheGlu 20
DB 185 ATCATCAAGGGGTTTCAGATGCAAGGCTCATCTCCAGAGCTGGCAGGAGCCCTGTCAG 244
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaIaProArgTyrPheLeuThrAla 40
DB 245 AAGAGCGGCGTCTCTGTGGGGCGACGCTCATCGCCCGCAATGGCTCTTCAGACAGCC 304
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 60
DB 305 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGCGACCACTCCAGAGAGAGAG 364
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisSerProGlyPheAsnAsnSer 80
DB 365 GGGTGTGACAGACCCGGGACCACTGATGCTCTCCCGCCAGAGAGAGAGAGAGAGAGAG 424
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCGCCCAACAAGACCAACCGCATGATCATGTGTGGAGAGAGAGAGAGAGAGAGAGAG 484
QY 101 IletThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 485 ATCACTGGGTGTGGCGACCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisSerThrLeu 140
DB 545 TGCCCTCATTTCCGGCTGGGGCGACAGCTCCAGCCCGCAATGAGAGAGAGAGAGAGAGAG 604
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 605 CGATGCGCCCAATCATCATCATGAGCAGCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 664
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnLysIleValLysAspSerCysGlnGly 180
DB 665 ATCAAGACCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTyrGlyGln 200
DB 725 GACATCGGGGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 784
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
DB 785 GATCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 844
QY 221 TrrIleGlnIleThrMetLysAsnAsn 229
DB 845 TGATTCAGAGAGAGATGAGAGAGAGAT 871

RESULT 2
US-10-205-823-211
/ Sequence 211, Application US/10205823
/ Publication No. US20030108963A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Endege, Wilson O.
```

```
APPLICANT: Gamavaramu Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamakkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Glat, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 4.2e-142      Length: 1186
Score: 1258.00          Matches: 229
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 15                  Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-205-823-211 (1-1186)

QY 1 IletlelySGlyPheGluCyslySProHisSerGlnProTPGlnAlaLeuPheGlu 20
DB 185 ATCATCAAGGGGTTTCAGATGCAAGGCTCATCTCCAGAGCTGGCAGGAGCCCTGTCAG 244
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaIaProArgTyrPheLeuThrAla 40
DB 245 AAGAGCGGCGTCTCTGTGGGGCGACGCTCATCGCCCGCAATGAGAGAGAGAGAGAGAGAG 304
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGln 60
DB 305 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGACCAACTCCAGAGAGAGAGAGAGAG 364
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisSerProGlyPheAsnAsnSer 80
DB 485 ATCACTGGGTGTGGCGACCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 425 CTCGCCCAACAAGACCAACCGCATGATCATGTGTGGAGAGAGAGAGAGAGAGAGAGAGAG 484
QY 101 IletThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 485 ATCACTGGGTGTGGCGACCCCTCACTCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisSerThrLeu 140
DB 545 TGCCCTCATTTCCGGCTGGGGCGACAGCTCCAGCCCGCAATGAGAGAGAGAGAGAGAGAGAG 604
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
DB 605 CGATGCGCCCAATCATCATCATGAGCAGCAAGAGTGTGAAGAGAGAGAGAGAGAGAGAGAG 664
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Qy 161 lIeThrAspThmMetValCysAlaSerValGlnGlnGlyGlyAspSerCysGlnGly 180  
Db 665 ATCAAGACCAATGGTGTGTGTCAGAGCAAGAGGAGACTCTCTCCAGAGGT 724  
Qy 181 AspSergIyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 725 GACTCCGGGGCCCTCTGTCTGTATACCAAGCTCTTCAAGCATTAATCTCTGGGGCCAG 784  
Qy 201 AspProCysAlaIleThrArgIleProGlyValIleThrIleValCysIleTyValAsp 220  
Db 785 GATCCGTGTGGATCAACCCGAAGCCTGTGTCTCAAGAAAGTCAATATATGTGAC 844  
Qy 221 TrpIleGlnIleThrMetIleAsnAsn 229  
Db 845 TCGATCCAGAGACGATGAAGACAAT 871

## RESULT 3

US-10-295-027-559  
Sequence 559, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:

APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glyne, Richard  
APPLICANT: Hevez, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
FILE REFERENCE: 018501-012500US  
CURRENT FILING DATE: US/10/295,027  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 559  
LENGTH: 1186  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-295-027-559

## Alignment Scores:

Pred. No.: 4.2e-142 Length: 1186  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-295-027-559 (1-1186)

Qy 1 lIeIleIyGlyPheGlyCysIleProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20  
Db 185 ATCATCAAGAGGCTTCAGAGCAAGCTCACTCCAGCCCTGGACAGCAGCCTGTTCAG 244  
Qy 21 lYsThrArgLeuLeuGlyValAlaThrIleuIleAlaProArgTrpLeuThrAlaAla 40  
Db 245 AAGACCGGCTACTCTGTGGGGCGAGCGCTCATCGCCCAAGATGGCTCTTGACAGAGCC 304  
Qy 41 HisCysLeuIleProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnGluGlu 60  
Db 305 CACTGCTCAAGCCCGCTACATAGTCACTGGGGCAGACCAACCTCCAGAGAGGAGAG 364  
Qy 61 GlyCysGlnGlnThrArgThrAlaThrIleuSerPheProHisSerGlnProGlyPheAsnSer 80  
Db 365 GGCTGTAGAGAGACCCGAGAGCCAGCCAGCTGAGTCTTCCACCCGAGCTTCACAGAGC 424  
Qy 81 LeuProAsnIleAspHisArgAsnAspIleMetLeuValIleMetAlaSerProValSer 100  
Db 425 CTCCCAACAAAGACCAAGCATGATCATGCTGTGAAGATGGCATGCGCAGCTCC 484  
Qy 101 lIeThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
Db 485 ATCACTGGAGCTGTGGACCCCTCACTCTCTCAAGCTGTCACTGTGGACAGC 544  
Qy 121 CysLeuIleSerGlyTrpIleSerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
Db 545 TGCTCATTTCCGGCTGGGGGAGAGAGCTCAAGCCCAATTAAGCTGCTCAAGCTTG 604  
Qy 141 ArgCysAlaAsnIleThrIleIleGluHisGlnIleCysGlnAsnAlaTyProGlyAsn 160  
Db 605 CGATGGCCCAACATCACTCATGAGCAGCAGAGTGAGAGAGCCCAACCCGCAAC 664  
Qy 161 lIeThrAspThmMetValCysAlaSerValGlnGlnGlyGlyAspSerCysGlnGly 180  
Db 665 ATCAAGACCAATGGTGTGTGTCAGAGCAAGAGGAGACTCTCTCCAGAGGT 724  
Qy 181 AspSergIyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 725 GACTCCGGGGCCCTCTGTCTGTATACCAAGCTCTTCAAGCATTAATCTCTGGGGCCAG 784  
Qy 201 AspProCysAlaIleThrArgIleProGlyValIleThrIleValCysIleTyValAsp 220  
Db 785 GATCCGTGTGGATCAACCCGAAGCCTGTGTCTCAAGAAAGTCAATATATGTGAC 844  
Qy 221 TrpIleGlnIleThrMetIleAsnAsn 229  
Db 845 TCGATCCAGAGACGATGAAGACAAT 871

## RESULT 4

US-10-173-999-159  
Sequence 159, Application US/10173999  
Publication No. US2004000563A1  
GENERAL INFORMATION:

APPLICANT: Gish, Kurt C.  
APPLICANT: Mack, David H.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions  
FILE REFERENCE: 018501-002420US  
CURRENT FILING DATE: US/10/173,999  
PRIOR FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: US 60/299,234  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: US 60/315,287  
PRIOR FILING DATE: 2001-08-27  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/372,246  
PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 163  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 159  
LENGTH: 1186  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-173-999-159

Alignment Scores:  
Pred. No.: 4,2e-142 Length: 1186  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-10-173-999-159 (1-1186)

QY 1 Iletlelysglypheglucyelysleprohisserglntrotrpinaalaaleupheglu 20  
DB 185 ATCATCAAGGGGTTGAGTGCAGACCTCATCCAGCCCTGGCGAGCCCTGTTGAG 244  
QY 21 LysThrArgLeuLeuCySGlyAlaThrleuileAlaProArgTPlleuLeuThraAla 40  
DB 245 AAGAGCGGCTACTCTGTGGGCGACGCTCATCCGCCCGAGTGGCTCTGACGAGCC 304  
QY 41 HisCysLeuLysProArgTyrIleValHisleuGlyGlnHisAsnLeuGlnLysGlu 60  
DB 305 CACTGCCCTCAAGCCCGGCTACATAGTTCACCTGGGCGAGCAACCTCCAGAGAGAG 364  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 365 GGCTGTGAGCAGACCCGAGACGACCTGAGTCTTCCGCCCGCTTCAACAAGAGC 424  
QY 81 LeuProAsnLysAspHisArgAsnAspIleuLeuValLysMetAlaSerProValSer 100  
DB 425 CTCCCAACAAGACACCGCATGACATGCTGTGGTGAAGATGAGCATGCGCTTCC 484  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 485 ATCACTGGGCTGTGGGCGACCCCTCACTCTCTCAAGCTGTGCACTGGCGGAGCAGC 544  
QY 121 CysleuIleSerGlyTTPGlySerThrSerSerProGlnLeuAlaGluLeuProHisThrLeu 140  
DB 545 TGCCCTATTTCCGGCTGGGCGAGCAGCTCCAGCCCGAGTACCTGCTCCACACCTTG 604  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsn 160  
DB 605 CGATGCCCAATCATCATCATATGAGCAGCAAGAGTGTGAGAGCGCTTACCCCGGAGC 664  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 180  
DB 665 ATCAACAGACACCATGTGTGTGTGCGACGCTGACAGAGAGAGGAGCTCTGCGAGGCT 724  
QY 181 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTPGlyGln 200  
DB 725 GACTCCGGGAGCCCTCTGGTGTGTGTAACAGTCTTTAAGGCAATTAATCTCTGGGAGCAG 784  
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220  
DB 785 GATCGGTGTGAGTACCCGAAAGCTGTGTCTACACGAAAGTCTCAATAATGTGAGC 844  
QY 221 TrpIleGlnGluThrMetLysAsn 229  
DB 845 TGGATCCAGAGACGATGAGACAAAT 871

# RESULT 5

US-09-946-374-169  
Sequence 169, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Boetstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099336  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099396  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627

Thu Jun 24 10:06:29 2004

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Page 5

PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30

PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:  
Pred. No.: 4,29e-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-946-374-169 (1-1204)

QY 1 Tlellelysglypnehtgucyslvysprohisserglnprotirpinaaaleuphegu 20  
Db 169 ATCATCAAGGGGTTTCAGTCAAGCTCCACGCTGAGGAGGCTGTTCAG 228  
QY 21 lvtthrtargtneueucysgalyatnrlleuila1ProrargtrpneueuThra1Aa1 40  
Db 229 AAGAGCGGCTACTCTGTGGGCGAGGCTATGCCCCAGATGGTCTCTGACAGGAGCC 288  
QY 41 HisCysleuylsProArgrYrilevalHisleuGlyGlnHisasnleuGlnysgIgu 60  
Db 289 CACTGCTCAAGCCCGGCTCATAGTTCACTGGGCGAGCAACTCCAGAAAGAGAG 348  
QY 61 GlyCysleuGlnThrtrgThralatnrgIuserPheprroHisproGlyPheasnanser 80

Db	349	GGCTGTGAGCAGACCCGGACAGCCACTGATGCTCTTCCCAACCCCGGCTTCACACAGC	408
Qy	81	LeuProAsnIysAspHisIstArgAsnAspIleMetLeuValIysMetAlaSerProValSer	100
Db	409	CTCCCAACAAACACACCGCAATGACATCACTGTGTGAAGATGGCATCCAGTCTCC	468
Qy	101	IleThrTPrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThrSer	120
Db	469	ATCACCTGGGCTGTGGACACCCCTCACCTCTCTCACGGCTGTGCATCGTCGACACAGC	528
Qy	121	CysMetIleSerGlyIrrpGlySerThrIserSerProGlnIleArgLeuProHisIleThleu	140
Db	529	TGCTCATTTCCGGCTGGGGACACAGTCACAGCCCACTTTCGCTCTCTCCACACCTTG	588
Qy	141	ArgCysAlaAsnIleThrIleIleGlnHisGlnIysCysGluAsnAlaTyrProGlyAsn	160
Db	589	CGATGGCCCAACATCCACATCATTTGAGCCACGAAGTGTGAGAACAGCTTACCCGGAC	648
Qy	161	IleThrAspIrrMetValCysAlaSerValGlnGlnGlyGlyIleAspSerCysGlnGly	180
Db	649	ATCACAGACACCATGTGTGTGTGCACGTGCAGAGAAAGGGCGAAGACTCTGCAAGGT	708
Qy	181	AspSerGlyGlyIrrProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTrrGlyGln	200
Db	709	GACCCCGGGGCCCTTGCTGTATCACAGTCTTCAAGCGATTATCTCTGGAGCCAG	768
Qy	201	AspProCysAlaIleIleThrIrrGlySerProGlyValIyrrThrIysValCysIysTyrValAsp	220
Db	769	GATCCGGTGCATCAACCCGAAAGCTGGTGTCTTACAGAAAGTGTGCMAATTATGTGGAC	828
Qy	221	TrrIleGlnGlyIrrMetIysAsnAsn	229
Db	829	TGGATCCAGAGACATGAGAAACAAT	855

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RESULT 6
US-10-015-395A-169
; Sequence 169, Application US/10015395A
; Publication No. US20040073015A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015.395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 169
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-395A-169

Alignment Scores:
Pred. No.:      4,29e-142
Score:          1258.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    100.00%

Length: 1204
Matches: 229
Conservative: 0
Mismatch: 0
Indels: 0

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DB:	12	Gaps:	0
US-09-856-320A-2_COPY_54_282	(1-229)	x US-10-015-395A-169	(1-1204)
OY	1	IlellelysglyPheglucyusyserProhisserGlnPcotpPglnAlaAlaLeuPheGlu	20
Dd	169	ATCATCAAGGGGTTCAGAGCGAACGCCCTACCTCCAGCCTTGAGGGCAGCCCTTTTGGAG	228
OY	21	LysThrArgLeuLeuCyseGlyAlaThrLeuIleAlaProArgTPLeuLeuThAlaAla	40
Dd	229	AAGAACC GGCTACTCTGTGGGGCGAGCCCTCACCGCCCCACAATGGCTCTTACAGCAGCC	288
OY	41	HicCyseLyuysProArgTyriIleValHisLeuGIyGlnHisAsnLeuGlnLyseGlu	60
Dd	289	CACGTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCGACAAACCTCCACAAAGAGAGAG	348
OY	61	GlyCyseGluGlnThrArgThrAlaThrGusSerPheProHisProGlyYPheaAsnAsnSer	80
Dd	349	GGCTGTGAGCAGACCCCGACACCCACTAGTCTTCCCCACCCCGGCTTAADAAAGC	408
OY	81	LeuProAsnLysAspHisArgAsnAspIleValIleValMetAlaSerProValSer	100
Dd	409	CTCCCCAACAAAGACCCAGCGAATACTACATGCTGGTAGGAAGATGGCATGCCCA GTTCC	468
OY	101	IleThrTryAlaValArgProLeuThrLeuSerSerArgCyseValThraAlaGlyThrSer	120
Dd	469	ATCACTGGGCTGTGGGACCTCTCACCTCTCTCTACGCTGTGTCACTGCTGGGACACAGC	528
OY	121	CysLeuIleSerGlyTPGlySerThrSerSerProGlnLeuValGLeuProHisTh-Leu	140
Dd	529	TGGCTCATTTCCGGCTGGGGGAGCAGCGTCCAGCCCCTCGATTACCGCTGCCACACCTTG	588
OY	141	ArgCyseAlaAsnIleThrIleIleGlnHisGlnLysCyseGluAsnAlaTyProGlyAsn	160
Dd	589	CGATGGCCCACTCACTCACTATTAGACACCGAAGTGTGAAAGCCTTACCCCGGCAC	648
OY	161	IleThrAspThrMetValCyseAlaSerValGlnGlnGlyIlyAspSerCyseGlnGly	180
Dd	649	ATCACAGACACACTGTGTGTGTGCCAGCGCGACGGAAGGGGCAAGGACTCTCTGCCAGGT	708
OY	181	AspSerGlyGlyProleuValCyseAsnGlnSerLeuGlnGlyIleIleSerTPGlyGln	200
Dd	709	GACTCCGGGGGCCCTCTGGTCTGTAAACAGTCTTCAAGGCATTACTCTTGSGGGCAG	768
OY	201	AspProCyseAlaIleThrArgLysProGlyValTYThruLysValCyseLysTYValASP	220
Dd	769	GATCCGCTGTCGATCACCCGAAAGCCTGGTGTCTTACAGAAAGCTGCCAATAATGTGAC	828
OY	221	TrpIleGlnGlyThrMetLysAsn	229
Dd	829	TGGATCCAGAGACGATGAGAACAT	855

RESULT 7  
US-10-147-493-505  
; Sequence 505, Application US/10147493  
; Publication No. US20040029217A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Pilavroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William



APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C345  
CURRENT APPLICATION NUMBER: US/10/147,493  
CURRENT FILING DATE: 2002-05-17  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-147-493-505

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-147-493-505 (1-1204)

QY 1 IleIleIleYsgIyPheGluCyAlsyProHisSerGlnProTrpGlnAlaIalaLeuPheGlu 20  
DB 169 ATCATCAAGGGGCTTGAAGTGAAGCTTCACTCCAGCCCTTGGCAGGCAAGCTTTCGAG 228  
QY 21 LysThraIgleuLeuCyGlyAlaThrIleuIleAlaProArgTrpLeuThrAlaAla 40  
DB 229 AAGACGGCGTACTCTGTGGGGCAGCGCTCATCGCCCAATGAGTGTCTGACAGCAGCC 288  
QY 41 HisCysLeuYsProArgTrpIleValHisIleuGlyGlnHisAsnIleuGlnGlu 60  
DB 289 CACTGCTCAAGCCCGCTGATAGTTCACCTGGGGCAGCAACCTCCAGAAAGAGAGAG 348  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GGCTGTGAGCAGACCCCGGACAGCACTGAGTCTTCCCGCCAGCCCGGCTTCAACACAGC 408  
QY 81 LeuProAsnIleAspHisArgAsnAspIleMetIleuValIysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACCCAGCAATGACATCATGTGTGAGAGATGGATCGCCAGTCTCC 468  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGGCAGCCCTTCACTCTCTCAAGCTGTGTCACTGTGGCAGCAGC 528  
QY 121 CysIleuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHisThrLeu 140  
DB 529 TGCTCATATTCGGGTGGGGCAGCAGCTCCAGCCCGCTTACCTGCTCAACACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleGlnHisGlnIleCysGlnAsnAlaIleProGlyAsn 160  
DB 589 CGATGCGCAACATCAACCATATGAGCAGCAAGAAAGTGTGAACGCTTACCCCGGCAAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValGlnIleGlyIlyAspSerCysGlnGly 180  
DB 649 ATCAAGACACCATGTGTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCGAGGCT 708  
QY 181 AspergilyGlyProLeuValCysAsnGlnSerIleuGlnIleIleSerTrpGlyGln 200  
DB 709 GACTCCGGGGGCGCTGTGTGTGAACCAAGTCTTCAAGGCAATTAATCTCTGGGGCCAG 768  
QY 201 AspProCysAlaIleThrArgIlyProGlyValIleThrIlyValCysIlyTyTrValAsp 220  
DB 769 GATCGGTGTGATACCCCGAAAGCTGTGTCTACAGAAAGTGTGAAATATGTGGAC 828  
QY 221 TrpIleGlnGluThrMetIlyAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAAACAAT 855  
RESULT 8

US-10-145-127-505  
Sequence 505, Application US/10145127  
Publication No. US20040033558A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smerwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C252  
CURRENT APPLICATION NUMBER: US/10/145,127  
CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-145-127-505

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-145-127-505 (1-1204)

QY 1 IleIleIleYsgIyPheGluCyAlsyProHisSerGlnProTrpGlnAlaIalaLeuPheGlu 20  
DB 169 ATCATCAAGGGGCTTGAAGTGAAGCTTCACTCCAGCCCTTGGCAGGCAAGCTTTCGAG 228  
QY 21 LysThraIgleuLeuCyGlyAlaThrIleuIleAlaProArgTrpLeuThrAlaAla 40  
DB 229 AAGACGGCGTACTCTGTGGGGCAGCGCTCATCGCCCAATGAGTGTCTGACAGCAGCC 288  
QY 41 HisCysLeuYsProArgTrpIleValHisIleuGlyGlnHisAsnIleuGlnGlu 60  
DB 289 CACTGCTCAAGCCCGCTGATAGTTCACCTGGGGCAGCAACCTCCAGAAAGAGAGAG 348  
QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GGCTGTGAGCAGACCCCGGACAGCACTGAGTCTTCCCGCCAGCCCGGCTTCAACACAGC 408  
QY 81 LeuProAsnIleAspHisArgAsnAspIleMetIleuValIysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACCCAGCAATGACATCATGTGTGAGAGATGGATCGCCAGTCTCC 468  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCACTGGGCTGTGGCAGCCCTTCACTCTCTCAAGCTGTGTCACTGTGGCAGCAGC 528  
QY 121 CysIleuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHisThrLeu 140  
DB 529 TGCTCATATTCGGGTGGGGCAGCAGCTCCAGCCCGCTTACCTGCTCAACACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnIleCysGlnAsnAlaIleProGlyAsn 160

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Db 589 CGATCGCGCAACATCCATCATGAGCAGGAGAGTGTGAAAGCGCTACCCCGGCGAC 648
Qy 161 ILeThAspThrMetValCysAlaSerValGlnGluGlyValYsAspSerCysGlnGly 180
Db 649 ATCAGACACCAATGATGTGTGTCAGCGCTGACAGAGAGGAGGAGACTCTCTGCAAGGCT 708
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 709 GACTCGGGGGCCCTCTGTCTGTAAACAGCTCTTCAAGGACATTACTCTGGGGGCGAG 768
Qy 201 AspProCysAlaIleThrArgValProGlyValIleThrIleValCysLysTrpValAsp 220
Db 769 GATCGGTGTGCGATCAGCCGGAAGCTGTGTCTAACAGAAAGTCTGCATAATATGTGAC 828
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGAGCATGAGAACAT 855

RESULT 9
US-10-160-503-505
; Sequence 505, Application US/10160303
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C446
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-160-503-505

Alignment Scores:
Pred. No.: 4,29e-142 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 13 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x US-10-160-503-505 (1-1204)
Qy 1 IleIleuysGlyPheGluCysLysPheHisSerGlnProTrpGlnAlaIleuPheGlu 20
Db 169 ATCATCAAGGGGTTGAGTGCAGACCTCCTCAGCCGCGGAGCGAGCCCTGTTGAG 228
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpPheLeuThrAlaIle 40
Db 229 AAGACGGCGCTACTGTGTGGGGGAGCGCTATCGCCCGAGATGGCTCTGACAGCGCC 288
Qy 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnGlyGlu 60
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Db 289 CACTGCTCAAGCCCCCGCTACATAGTTCACCTGSGGCGACACMACCTCCAGAAAGAGAG 348
Qy 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisSerProGlyPheAsnAsnSer 80
Db 349 GGCTGTGACACACCGCGAGCAGCCACTAGTCTCTCCCGACCCCGGCTTCAACAGAGC 408
Qy 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCCCCCAAAAGACACCGCAGATGACATCAGCTGGAGTGAAGATGGATCCGCACTCC 468
Qy 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 469 ATCAGCTGGGCTGTGTGAGACCCCTCAGCTCTCTCTCAACCTGTGTACCTGTGCGACCGAG 528
Qy 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 529 TGCTTCATTTCCGGCTGGGGGCGAGCGTCCAGCCCGCCAGTTACGCTCCTCAGCCCTTG 588
Qy 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlyAsnAlaTrpProGlyAsn 160
Db 589 CGATGCGCCACATACATCATCTAGACACAGAGTGTGAGAACGCTTACCCCGGCGAC 648
Qy 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyValYsAspSerCysGlnGly 180
Db 649 ATCAGACACCAATGATGTGTGTCAGCGCTGACAGAGAGGAGGAGGAGACTCTGCGAGGCT 708
Qy 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 709 GACTCGGGGGCCCTCTGTCTGTAAACAGCTCTTCAAGGACATTACTCTGGGGGCGAG 768
Qy 201 AspProCysAlaIleThrArgValProGlyValIleThrIleValCysLysTrpValAsp 220
Db 769 GATCCGTGTGCGATCAGCCGGAAGCTGTGTCTAACAGAAAGTCTGCATAATATGTGAC 828
Qy 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGAGCATGAGAACAT 855

RESULT 10
US-10-143-118-505
; Sequence 505, Application US/10143118
; Publication No. US20040038335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C228
; CURRENT APPLICATION NUMBER: US/10/143,118
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-143-118-505
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Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-10-144-993-505 (1-1204)

QY 1 IlelelysglypnehuCyselysProhisSerGlnProtrpGlnAlaLeuphegu 20  
Db 169 ATCATCAAGGGGTTGAGTGCACACCTTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 228

QY 21 lvsThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuLeuThraAla 40  
Db 229 AAGACGGCGCTACTGTGGGGCAGCGCTCATGCCGCCAGATGGCTCTGCACAGCAGCC 288

QY 41 HisCysleuysProArgTrpIleValHisleuGlyGlnHisAsnleuGlnLysGluGlu 60  
Db 289 CACTGCTCAAGCCCGCTTACATAGTTCACTGGGGCAGCACAACCTCCAGAGAGAG 348

QY 61 GlyCysGlnGlnThrArgThraAlaThrgIuserPheProhisProGlyPheAsnAsnSer 80  
Db 349 GCGTGTGAGCAGACCCGGAGCAGCACTGATGCTTCCCGCCAGCCCGGCTTCAACACAGC 408

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 409 CTCCCAACAAAGACCCAGCAGATGATCATGTGGAGATGGATGGCATGCCAGTCTCC 468

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThraAlaGlyThrsSer 120  
Db 469 ATCACTGGGCTGTGGCAGCCCTCACTTCTCACTGCTGTGCATGCTGGCAGCAGC 528

QY 121 CysleuIleSerGlyTrpGlySerThrsSerSerProGlnleuArgLeuProhisThrsLeu 140  
Db 529 TGCTCATATTCGGGTGGGGCAGCAGCTGCCAGCCCGCTTCACTGCTCAACACCTTG 588

QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaIleProGlyAsn 160  
Db 589 CGATGCCCAACATCAATCATTTAGAGCAGCAAGTGTGAAAGCGCTTACCCCGCAGAC 648

QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180  
Db 649 ATCAGACACCATGTGTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCCAGAGGT 708

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 709 GACTCGGGGGCCCTGTGGTGTGTAACAGTCTCTCAAGGCATTTATCTCTGGGGCCAG 768

QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrsLysValCysLysTrpValAsp 220  
Db 769 GATCGGTGTGGATACCCGAAAGCTGTGTCTACAGAAAGTGTGAATATGTGAGC 828

QY 221 TrpIleGlnGlnThrMetLysAsnAsn 229  
Db 829 TGGATCCAGAGACGATGAGAAACAAAT 855

RESULT 11  
US-10-144-993-505  
; Sequence 505, Application US/10144993  
; Publication No. US2004003836A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C261  
CURRENT APPLICATION NUMBER: US/10/144,993  
CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien

US-10-144-993-505

Alignment Scores:  
Pred. No.: 4,296-142 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-10-144-993-505 (1-1204)

QY 1 IlelelysglypnehuCyselysProhisSerGlnProtrpGlnAlaLeuphegu 20  
Db 169 ATCATCAAGGGGTTGAGTGCACACCTTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 228

QY 21 lvsThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuLeuThraAla 40  
Db 229 AACACGGCGCTACTGTGGGGCAGCGCTCATGCCGCCAGATGGCTCTGCACAGCAGC 288

QY 41 HisCysleuysProArgTrpIleValHisleuGlyGlnHisAsnleuGlnLysGluGlu 60  
Db 229 AACACGGCGCTACTGTGGGGCAGCGCTCATGCCGCCAGATGGCTCTGCACAGCAGC 288

QY 61 GlyCysGlnGlnThrArgThraAlaThrgIuserPheProhisProGlyPheAsnAsnSer 80  
Db 289 CACTGCTCAAGCCCGCTTACATAGTTCACTGGGGCAGCACAACCTCCAGAGAGAG 348

QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
Db 349 GCGTGTGAGCAGACCCGGAGCAGCACTGATGCTTCCCGCCAGCCCGGCTTCAACACAGC 408

QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThraAlaGlyThrsSer 120  
Db 469 ATCACTGGGCTGTGGCAGCCCTCACTTCTCACTGCTGTGCATGCTGGCAGCAGC 528

QY 121 CysleuIleSerGlyTrpGlySerThrsSerSerProGlnleuArgLeuProhisThrsLeu 140  
Db 529 TGCTCATATTCGGGTGGGGCAGCAGCTGCCAGCCCGCTTCACTGCTCAACACCTTG 588

QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaIleProGlyAsn 160  
Db 589 CGATGCCCAACATCAATCATTTAGAGCAGCAAGTGTGAAAGCGCTTACCCCGCAGAC 648

QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180  
Db 649 ATCAGACACCATGTGTGTGCCAGCTGCAGAGAGGGGCAAGAGACTCTGCCAGAGGT 708

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200  
Db 709 GACTCGGGGGCCCTGTGGTGTGTAACAGTCTCTCAAGGCATTTATCTCTGGGGCCAG 768

QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrsLysValCysLysTrpValAsp 220  
Db 769 GATCGGTGTGGATACCCGAAAGCTGTGTCTACAGAAAGTGTGAATATGTGAGC 828





```

APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C60
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 185
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-535-185

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```

Alignment Scores:
Pred. No.: 4,298-142 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

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US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-10-219-535-185 (1-1204)

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QY 1 Iletlelysglypnehlcyalsyprohisserglnprotglnalalaieuheglu 20
DB 169 ATCATCAAGGGGCTTGGAGTGCAGAGCTCACTCCAGCCCTGGAGGAGCCCTGTGAG 228
QY 21 LysThrArgLeuLeuCySGlyAlaThrlleuilealaproargtprleuLeuThraAla 40
DB 229 AAGAGCGGCGCTACTGTGGGCGAGCGCTCAATGCCGCCCAATGAGCTCTCCAGCGAGCC 288
QY 41 HisCysLeuLysProArgTyrIleValHisLeuLysLysLysLysLysLysLysLysLys 60
DB 289 CACTCCCTCAAGCCCGGCTCATATGATTCCTGGGCGAGCAACCTCCAGAGAGAGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrlGluSerPheProHisPProGlyPheAsnAsnSer 80
DB 349 GAGCTGTGAGACCCCGGAGCGAGCACTGAGTCTTCCGCCCAAGGCTTCAACAGAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleLeuLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCAACAAGACCAAGCAATGACATCTGCTGTGAAGATGCGATGCCAGTCTCC 468
QY 101 IletThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120

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DB 469 ATCACTGGGCTTGGAGCCCTCACTCTCTCAAGCTGTCTACTGTGACACCAAG 528
QY 121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 529 TGCCTCATTTCCCGCTGGGCGAGCAGCTCAGAGCCCAATTCAGCTGCTCAGACCTTG 588
QY 141 ArgCysAlaAsnLethrIlelleGluHisLysCysGluAsnAlaTyrProGlyAsn 160
DB 589 CGATGGCCCAACATCCATATTGAGCCCAAGTGTGAAGACCTTACCCCGGAGAC 648
QY 161 IletThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 649 ATCAAGACACCATGTGAGTGTGCAGCGAGGAAGGGGCAAGAGACTCTGCCAGGGT 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIlelleSerTrpGlyGln 200
DB 709 GACTCCGGGGGCTTGTGTGTGTACAGTCTTCAAGGATTAATCTCCGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLysPProGlyValIleThrLysValCysLysTyrValAsp 220
DB 769 GATCCGTGTGCATCAACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 828
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 829 TGGATCCAGAGAGCATGAAGAAACAT 855

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# RESULT 15

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US-10-232-230-185
Sequence 185, Application US/10232230
Publication No. US20040044180A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C103
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 185
LENGTH: 1204
TYPE: DNA

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ORGANISM: Homo Sapien  
US-10-232-230-185

## Alignment Scores:

Pred. No.:	4.29e-142	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-232-230-185 (1-1204)

```
QY      1 11e1leysglyPheglucylsPProHisserGlnProTropAlaAlaLeupheGlu 20
          |||||
Db      169 ATCATCAAGGGGCTCGAGTGCAGAGCTCATCCAGCCCTGGCAGGCGAGCCCTGTTGAG 228

QY      21 LysThrArgLeuLeuGlyAlaThrLeu11eAlaProArgTProLeuThrAlaAla 40
          |||||
Db      229 AAGACGGGGCTACTCTGTGGGGCAGCCCTCATCGCCCGCATGGCTCTGACAGAGCC 288

QY      41 HisCysLeuLysProArgTyr11eAlaHisLeuGlyGlnHisLeuGlnLysGluGlu 60
          |||||
Db      289 CACTGCTCAAGCCCGCTCATAGTTCACCTGGGGCAGCACAACCTCCAGAGGAGAG 348

QY      61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
          |||||
Db      349 GGCTGTAGAGCAGACCCGAGCAGCCAGCTGAGCTTCCCCACCCGGCTTCAACACAGC 408

QY      81 LeuProAsnLysAspHisArgAsnAsp11eLeuLeuValLysMetAlaSerProValSer 100
          |||||
Db      409 CTCCCAACAAAGACCAACCGAATGACATCAAGCTGTGAAGATGCAATGCCAGTCTCC 468

QY      101 11eThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
          |||||
Db      469 ATCACTGGGGCTGTGGCAGCCCTCACCCCTCTCCACGCTGTGTCACTGGGACCCAGC 528

QY      121 CysLeuLysSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
          |||||
Db      529 TGCTCTATTTCGGGCTGGGGCAGCAGCTCCAGCCCGCATGACGCTGCTCACACCTTG 588

QY      141 ArgCysAlaAsn11eThr11eGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
          |||||
Db      589 CGATGCCGCCAATCATCAATCATGAGACCAAGAGTGTGGAACGGCTACCCCGGCAAC 648

QY      161 11eThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
          |||||
Db      649 ATCAACAGACACCATGTGTGTGTGCCAGCGTGCAGAGAGGGGCAAGACTCTGTCCAGGGT 708

QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly11e11eSerTrpGlyGln 200
          |||||
Db      709 GACTCCGGGGGCGCTCTGTGTGTGTACCAAGTCTCTTCAAGGCATTATCTCTGGGGCCAG 768

QY      201 AspProCysAla11eThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
          |||||
Db      769 GATCGGTGTGCAATCAACCGAAAGCTGTGTCTACAGAAAGTCTCAAAATATGTGAC 828

QY      221 Trp11eGlnGluThrMetLysAsnAsn 229
          |||||
Db      829 TGGATCCAGAGAGATGAAGAACAAT 855
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Search completed: June 23, 2004, 04:01:35  
Job time : 486 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 22, 2004, 18:54:57 ; Search time 48 Seconds  
(Without alignments)  
1346.871 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IITGFCCKPHSPQWAALE.....GYTVKCKYVDWIQETMKNN 229

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 28213646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubppaa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubppaa/PCFUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
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11: /cgn2\_6/prodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
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13: /cgn2\_6/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
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16: /cgn2\_6/prodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1258	100.0	US-09-946-374-170	Sequence 170, App
2	1258	100.0	US-09-933-767-427	Sequence 427, App
3	1258	100.0	US-10-147-493-506	Sequence 506, App
4	1258	100.0	US-10-145-127-506	Sequence 506, App
5	1258	100.0	US-10-160-503-506	Sequence 506, App
6	1258	100.0	US-10-143-118-506	Sequence 506, App
7	1258	100.0	US-10-144-993-506	Sequence 506, App
8	1258	100.0	US-10-158-787-506	Sequence 506, App
9	1258	100.0	US-10-081-056-208	Sequence 208, App
10	1258	100.0	US-10-219-535-186	Sequence 186, App
11	1258	100.0	US-10-232-330-186	Sequence 186, App
12	1258	100.0	US-10-140-024-506	Sequence 506, App
13	1258	100.0	US-10-140-808-506	Sequence 506, App
14	1258	100.0	US-10-004-860-427	Sequence 427, App
15	1258	100.0	US-10-006-485A-170	Sequence 170, App

#### ALIGNMENTS

16	1258	100.0	250	12	US-10-013-907A-170	Sequence 170, App
17	1258	100.0	250	12	US-10-015-499A-170	Sequence 170, App
18	1258	100.0	250	12	US-10-232-324-186	Sequence 186, App
19	1258	100.0	250	12	US-10-013-510A-170	Sequence 170, App
20	1258	100.0	250	12	US-10-152-405-506	Sequence 506, App
21	1258	100.0	250	12	US-10-127-852A-506	Sequence 506, App
22	1258	100.0	250	12	US-10-127-900A-506	Sequence 506, App
23	1258	100.0	250	12	US-10-128-685A-506	Sequence 506, App
24	1258	100.0	250	12	US-10-226-354A-170	Sequence 170, App
25	1258	100.0	250	12	US-10-131-820A-506	Sequence 506, App
26	1258	100.0	250	12	US-10-142-886-506	Sequence 506, App
27	1258	100.0	250	12	US-10-146-128-506	Sequence 506, App
28	1258	100.0	250	12	US-10-146-786-506	Sequence 506, App
29	1258	100.0	250	12	US-10-147-499-506	Sequence 506, App
30	1258	100.0	250	12	US-10-157-798-506	Sequence 506, App
31	1258	100.0	250	12	US-10-305-654A-208	Sequence 208, App
32	1258	100.0	250	12	US-10-015-395A-170	Sequence 170, App
33	1258	100.0	250	14	US-10-028-072-506	Sequence 506, App
34	1258	100.0	250	14	US-10-121-049-506	Sequence 506, App
35	1258	100.0	250	14	US-10-123-904-506	Sequence 506, App
36	1258	100.0	250	14	US-10-140-470-506	Sequence 506, App
37	1258	100.0	250	14	US-10-175-746-506	Sequence 506, App
38	1258	100.0	250	14	US-10-176-918-506	Sequence 506, App
39	1258	100.0	250	14	US-10-176-921-506	Sequence 506, App
40	1258	100.0	250	14	US-10-227-884-186	Sequence 186, App
41	1258	100.0	250	14	US-10-137-865-506	Sequence 506, App
42	1258	100.0	250	14	US-10-140-474-506	Sequence 506, App
43	1258	100.0	250	14	US-10-142-431-506	Sequence 506, App
44	1258	100.0	250	14	US-10-143-114-506	Sequence 506, App
45	1258	100.0	250	14	US-10-230-163-186	Sequence 186, App

RESULT 1  
US-09-946-374-170  
Sequence 170, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750



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PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1258; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQPQALFFETRLCGATLIAPRMILTAHCKPRYIVHLSGHNIQKE 60
DB 22 IIKGFCEKPHSQPQALFFETRLCGATLIAPRMILTAHCKPRYIVHLSGHNIQKE 81
QY 61 GCEOTRATESFPHPGNNSLPNKDHNDIMLVMA SPASITVA RPLTSSRCVTAAGTS 120
DB 82 GCEOTRATESFPHPGNNSLPNKDHNDIMLVMA SPASITVA RPLTSSRCVTAAGTS 141
QY 121 CLISGWSTSSPOLRPHTRCANITIEHOKCENAYPNTITWVCASVOEGSKDSCQG 180
DB 142 CLISGWSTSSPOLRPHTRCANITIEHOKCENAYPNTITWVCASVOEGSKDSCQG 201
QY 181 DSGGPIVNCNLSGIIISMGDPCATIRKPGVITVCYVNMIOETMKN 229
DB 202 DSGGPIVNCNLSGIIISMGDPCATIRKPGVITVCYVNMIOETMKN 250

RESULT 2
US-09-933-767-427
Sequence 427; Application us/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007B2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,836
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US98/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,880
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,896
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,020
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,876

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PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,895
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,884
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,894
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,971
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,882
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,899
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,893
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,900
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,901
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,892
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,915
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,019
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,972
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,916
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,373
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,875
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,374
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,917
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,949
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,974
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,883
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,897
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,898
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,962
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,963
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,877
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,878
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,064
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,053
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30

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PRIOR APPLICATION NUMBER: 60/073,164  
PRIOR FILING DATE: 1998-01-30  
PRIOR APPLICATION NUMBER: 60/085,925  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,921  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,923  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/085,922  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: 60/092,921  
PRIOR FILING DATE: 1998-07-15  
PRIOR APPLICATION NUMBER: 60/094,657  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1245  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 427  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-933-767-427

Query Match 100.0%; Score 1258; DB 10; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 60  
DB 22 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 81  
QY 61 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRPLHTLRCAVITIIHQKCNAYPGNITDTMVCASVQEGKXSCQG 180  
DB 142 CLISGSGTSSPOLRPLHTLRCAVITIIHQKCNAYPGNITDTMVCASVQEGKXSCQG 201  
QY 181 DSGGPLVNCNOSLQGIISWGQDPCATRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLQGIISWGQDPCATRKPGVYTVCKYVDMIOETMKN 250

RESULT 3  
US-10-147-493-506  
Sequence 506, Application US/10147493  
Publication No. US20040029217A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Mei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C345  
CURRENT APPLICATION NUMBER: US/10/147,493  
CURRENT FILING DATE: 2002-05-17  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506

LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-147-493-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 60  
DB 22 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 81  
QY 61 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRPLHTLRCAVITIIHQKCNAYPGNITDTMVCASVQEGKXSCQG 180  
DB 142 CLISGSGTSSPOLRPLHTLRCAVITIIHQKCNAYPGNITDTMVCASVQEGKXSCQG 201  
QY 181 DSGGPLVNCNOSLQGIISWGQDPCATRKPGVYTVCKYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLQGIISWGQDPCATRKPGVYTVCKYVDMIOETMKN 250

RESULT 4  
US-10-145-127-506  
Sequence 506, Application US/10145127  
Publication No. US2004003358A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Mei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C345  
CURRENT APPLICATION NUMBER: US/10/145,127  
CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-145-127-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 60  
DB 22 IIKGECKPHSQPQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGCHNLOKEE 81  
QY 61 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATESFPHPGFNNSLPNKDHNDIMLVKASPVSIITVAVRPLTSSRCVTAGTS 141

QY 121 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 180  
 DB 142 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 201  
 QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 229  
 DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 250

## RESULT 5

US-10-160-503-506  
 ; Sequence 506, Application US/10160503  
 ; Publication No. US20040035559A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C228  
 ; CURRENT FILING DATE: 2002-05-30  
 ; CURRENT APPLICATION NUMBER: US/10/160,503  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 506  
 ; LENGTH: 250  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-160-503-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQWQALFEKTRLLCGATLIAPRWLLTAHCKRPRIYVHIGQHNLOKKE 60  
 DB 22 IIKGFCEKPHSQWQALFEKTRLLCGATLIAPRWLLTAHCKRPRIYVHIGQHNLOKKE 81  
 QY 61 GCEQRTATSPFPHGFNNLSLPKNDHNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSPFPHGFNNLSLPKNDHNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 141  
 QY 121 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 180  
 DB 142 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 201  
 QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 229  
 DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 250

## RESULT 6

US-10-143-118-506  
 ; Sequence 506, Application US/10143118  
 ; Publication No. US20040038335A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C228  
 ; CURRENT FILING DATE: 2002-05-09  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 506  
 ; LENGTH: 250  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-143-118-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCEKPHSQWQALFEKTRLLCGATLIAPRWLLTAHCKRPRIYVHIGQHNLOKKE 60  
 DB 22 IIKGFCEKPHSQWQALFEKTRLLCGATLIAPRWLLTAHCKRPRIYVHIGQHNLOKKE 81  
 QY 61 GCEQRTATSPFPHGFNNLSLPKNDHNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 120  
 DB 82 GCEQRTATSPFPHGFNNLSLPKNDHNDIMLVKMASPVSIITWAVPLTSSRCVTAGTS 141  
 QY 121 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 180  
 DB 142 CLISGSGSTSSPOLRLPHTLRCAANTITIEHOKCENAYPGNITDTWVCASVOEGGKDSGCG 201  
 QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 229  
 DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 250

## RESULT 7

US-10-144-993-506  
 ; Sequence 506, Application US/10144993  
 ; Publication No. US20040038336A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C261  
 ; CURRENT APPLICATION NUMBER: US/10/144,993

CURRENT FILING DATE: 2002-05-13  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-144-993-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQTRATESFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQTRATESFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITITIEHQKCNAPGNITDTMVCASVOEGKDCSCG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITITIEHQKCNAPGNITDTMVCASVOEGKDCSCG 201  
QY 181 DSGGPLVNCQSLQGIISWGODPCAITRKPGYTVKCYVDMIOETMKN 229  
DB 202 DSGGPLVNCQSLQGIISWGODPCAITRKPGYTVKCYVDMIOETMKN 250

RESULT 8  
US-10-158-787-506  
Sequence 506, Application US/10158787  
Publication No. US20040039164A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C49  
CURRENT APPLICATION NUMBER: US/10/158,787  
CURRENT FILING DATE: 2003-04-03  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or Palm.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-158-787-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 60  
DB 22 IIKGFECKPHSQPQWALFEKTRLLCGATLIAPRWMLTAHCKPRYIVHLGQHNLOKEE 81  
QY 61 GCEQTRATESFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 120  
DB 82 GCEQTRATESFPHPGFNNSLPNKDHNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITITIEHQKCNAPGNITDTMVCASVOEGKDCSCG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITITIEHQKCNAPGNITDTMVCASVOEGKDCSCG 201  
QY 181 DSGGPLVNCQSLQGIISWGODPCAITRKPGYTVKCYVDMIOETMKN 229  
DB 202 DSGGPLVNCQSLQGIISWGODPCAITRKPGYTVKCYVDMIOETMKN 250

RESULT 9  
US-10-081-056-208  
Sequence 208, Application US/10081056  
Publication No. US20040043927A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Geiber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillari, Kenneth J.  
APPLICANT: Marsters, Scott A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilian  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
FILE REFERENCE: P335P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17

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PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 208
LENGTH: 250
TYPE: PRT
ORGANISM: Homosapiens
US-10-081-056-208

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Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 60
Db 22 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 81
Qy 61 GGEQRTATSEFPHPGFNNSLBNKDHNDIMLVMAASPVSLTMAVRPLTLSSRCVTAGTS 120
Db 82 GGEQRTATSEFPHPGFNNSLBNKDHNDIMLVMAASPVSLTMAVRPLTLSSRCVTAGTS 141
Qy 121 CLISMGSTSSPOLRPLTLTLCANITIIHCKCENAYFGNITDTMVCASVGGKDSGCG 180
Db 142 CLISMGSTSSPOLRPLTLTLCANITIIHCKCENAYFGNITDTMVCASVGGKDSGCG 201
Qy 181 DSGGPLVNCQSLGFIISWGDPICALTRPGYTVYVCKYVDWIOETMKN 229
Db 202 DSGGPLVNCQSLGFIISWGDPICALTRPGYTVYVCKYVDWIOETMKN 250

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RESULT 10
US-10-219-535-186
Sequence 186, Application US/10219535
Publication No. US20040044179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerilsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Warabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC60
CURRENT APPLICATION NUMBER: US/10/219,535
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 186
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-535-186

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Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 60
Db 22 IIKGECKPHSQPWOALFEKTRLLCGATLLAPRWLLTAACLKPRYIVHLGQNLQKEE 81

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QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 250

RESULT 11  
US-10-232-230-186  
; Sequence 186, Application US/102322230  
; Publication No. US20040044180A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerltsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C103  
; CURRENT APPLICATION NUMBER: US/10/232.230  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 186  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-232-230-186

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKKE 60  
DB 22 IIKGFCKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKKE 81  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 201

DB 82 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 250

RESULT 12  
US-10-140-024-506  
; Sequence 506, Application US/10140024  
; Publication No. US20040058424A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zhenli  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C69  
; CURRENT APPLICATION NUMBER: US/10/140.024  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or file wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 506  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-024-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKKE 60  
DB 22 IIKGFCKPHSQPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKKE 81  
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 120  
DB 82 GCEQRTATSEFPHPGFNNSLPNKDHNDIMLVMAASPVSIITVAVRPLTSSRCVTAGTS 141  
QY 121 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 180  
DB 142 CLISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAPGNITDTMVCASVOEGGKDCSCOG 201  
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 229  
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRKPGVYTKVCYVDMIOETMKN 250

RESULT 13  
US-10-140-808-506  
; Sequence 506, Application US/10140808  
; Publication No. US20030017563A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.



APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin J.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P33081C182  
CURRENT APPLICATION NUMBER: US/10/140,808  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-808-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQWQALFEKTRLLCGATLIAAPWLLTAACLKERYIVHIGQHNQKEE 60  
DB 22 IIKGFCKPHSQWQALFEKTRLLCGATLIAAPWLLTAACLKERYIVHIGQHNQKEE 81  
QY 61 GCEQRTATSFPHGPNNSLPKXDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 120  
DB 82 GCEQRTATSFPHGPNNSLPKXDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 141  
QY 121 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGKDSQCG 180  
DB 142 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGKDSQCG 201  
QY 181 DSGGPLVNCOSLQGIISWGQDPCATRRKPGVYTKVKCYVDWIOETMKN 229  
DB 202 DSGGPLVNCOSLQGIISWGQDPCATRRKPGVYTKVKCYVDWIOETMKN 250

RESULT 14  
US-10-004-860-427  
Sequence 427, Application US/10004860  
Publication No. US20030065160A1  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/10/004,860  
CURRENT FILING DATE: 2001-12-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-004-860-427

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1,4e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQWQALFEKTRLLCGATLIAAPWLLTAACLKERYIVHIGQHNQKEE 60  
DB 22 IIKGFCKPHSQWQALFEKTRLLCGATLIAAPWLLTAACLKERYIVHIGQHNQKEE 81  
QY 61 GCEQRTATSFPHGPNNSLPKXDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 120  
DB 82 GCEQRTATSFPHGPNNSLPKXDRNDIMLVKASVSIITWAVPLTSSRCVTAAGTS 141  
QY 121 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGKDSQCG 180  
DB 142 CLISGSGTSSPOLRPLTLRCANITIIHQKCNAYPGNITDTWVCASVQEGKDSQCG 201  
QY 181 DSGGPLVNCOSLQGIISWGQDPCATRRKPGVYTKVKCYVDWIOETMKN 229  
DB 202 DSGGPLVNCOSLQGIISWGQDPCATRRKPGVYTKVKCYVDWIOETMKN 250

RESULT 15  
US-10-006-485A-170  
Sequence 170, Application US/10006485A  
Publication No. US20030064062A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C9  
CURRENT APPLICATION NUMBER: US/10/006,485A  
CURRENT FILING DATE: 2001-12-06  
Prior Application Number: 60/095716  
Prior Filing Date: 1998-09-01  
Prior Application Number: 60/098723  
Prior Filing Date: 1998-09-01  
Prior Application Number: 60/098749  
Prior Filing Date: 1998-09-01  
Prior Application Number: 60/098750  
Prior Filing Date: 1998-09-01  
Prior Application Number: 60/098803  
Prior Filing Date: 1998-09-02  
Prior Application Number: 60/098821  
Prior Filing Date: 1998-09-02  
Prior Application Number: 60/098843  
Prior Filing Date: 1998-09-02  
Prior Application Number: 60/099336  
Prior Filing Date: 1998-09-09  
Prior Application Number: 60/099366  
Prior Filing Date: 1998-09-09  
Prior Application Number: 60/099741  
Prior Filing Date: 1998-09-10  
Prior Application Number: 60/099754  
Prior Filing Date: 1998-09-10  
Prior Application Number: 60/099763  
Prior Filing Date: 1998-09-10  
Prior Application Number: 60/099792  
Prior Filing Date: 1998-09-10



Query Match 100.0%; Score 1258; DB 12; Length 250;  
 Best Local Similarity 100.0%; Pred.No.1,4e-116;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	IIKGFCKPHSQPWQALFEKTRILCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE	60
DB	22	IIKGFCKPHSQPWQALFEKTRILCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE	81
QY	61	GCEQRTATSESPHPGPNNSLPNKDHRNDIMLVKASPVSTAVRPLTLSSRCTAGTS	120
DB	82	GCEQRTATSESPHPGPNNSLPNKDHRNDIMLVKASPVSTAVRPLTLSSRCTAGTS	141
QY	121	CLISGWGSTSSPOLRLPHLTRCANITIIHOKCENAYPGNITDTWVCASVQEGKDSCOG	180
DB	142	CLISGWGSTSSPOLRLPHLTRCANITIIHOKCENAYPGNITDTWVCASVQEGKDSCOG	201
QY	181	DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	229
DB	202	DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	250

Search completed: June 22, 2004, 18:58:28  
 Job time : 49 secs

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